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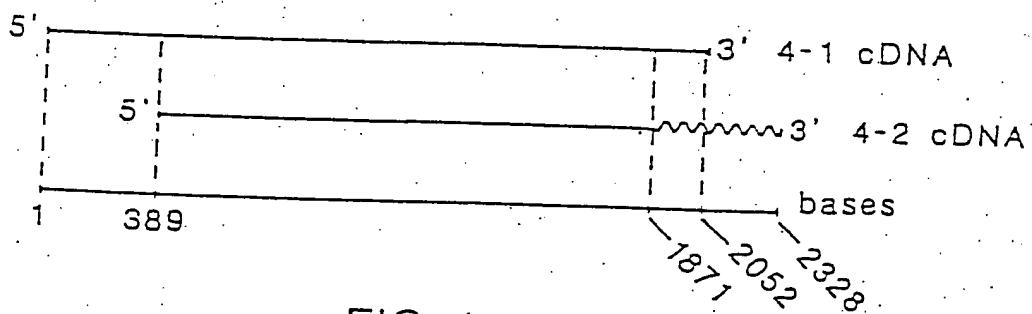


FIG. 1



GGC ACC GGG 10 GCG CCG CCG CCG CTG CTG CTA 30 CTG CCG CTG CTG CTG CTC CTA 50 GGG ACC GGC
Gly Thr Gly Ala Pro Pro Pro Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu Gly Thr Gly

CTC TTG CCT 70 GCT AGC AGC CAC ATA GAG ACC 90 CCG GCC CAT GCG GAG GAG 110 CCG CTC CTG AAG
Leu Leu Pro Ala Ser Ser His Ile Glu Thr Arg Ala His Ala Glu Glu Arg Leu Leu Lys

AGA CTC TTC TCC 130 GGT TAC AAC AAG TGG TCT CCG CCA GTA GGC AAT ATC 170 TCA GAT GTG GTC
Arg Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg Pro Val Gly Asn Ile Ser Asp Val Val

CTC GTC CCG TTT 190 GGC TTG TCC ATT GCT CAG CTC ATT GAC GTG GAC 230 GAG AAG AAC CAG ATG
Leu Val Arg Phe Gly Leu Ser Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met

ATG ACA ACC AAC 250 GTG TGG GTG AAG CAG GAG TGG CAC GAC TAC AAG CTG 290 CCG TGG GAC CCT
Met Thr Thr Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp Pro

GGT GAC TAC GAG AAT 310 GTC ACC TCC ATC 330 CCG ATC CCC TCT GAA CTC ATC TGG AGG CCT GAC
Gly Asp Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu Ile Trp Arg Pro Asp

ATC GTC CTC TAC AAC AAT 370 GCG GAT GGA GAC TTT GCA GTC ACC CAC CTG 410 ACC AAG GCC CAC
Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe Ala Val Thr His Leu Thr Lys Ala His

CTG TTC TAT GAC 430 GGA AGG GTG CAG TGG 450 ACA CCC CCA GCC ATC TAT AAG AGC TCC TGC AGC
Leu Phe Tyr Asp Gly Arg Val Gln Trp Thr Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser

ATC GAC GTC ACC TTC TTC 490 CCC TTT GAC CAG CAG AAC TGT ACC ATG AAG TTT 530 GGA TCC TGG
Ile Asp Val Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Thr Met Lys Phe Gly Ser Trp

ACC TAC GAC AAG GCC AAG ATT GAC TTA 570 GTG AGC ATT CAT AGC CGT GTG GAC CAA CTG GAC
Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Ile His Ser Arg Val Asp Gln Leu Asp

TTC TGG GAA AGT 610 GGG GAG TGG GTC ATC 630 GTG GAT GCT GTG GGC ACC TAC AAC ACC AGG AAG
Phe Trp Glu Ser Gly Glu Trp Val Ile Val Asp Ala Val Gly Thr Tyr Asn Thr Arg Lys

TAC GAG TGC TGT 670 GCC GAG ATC TAT CCT GAC ATC ACC TAT GCC TTC ATC ATC 710 CCA CCG CTG
Tyr Glu Cys Cys Ala Glu Ile Tyr Pro Asp Ile Thr Tyr Ala Phe Ile Ile Arg Arg Leu

CCG CTA TTC TAC ACC ATC AAC CTC ATC ATC 730 CCG TGC CTG CTC ATC TCC TGT CTC ACC GTG
Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr Val

FIG. 2A



790
CTG GTC TTC TAT CTG CCT TCA GAG TGT 810
Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Val Thr Leu Cys Ile Ser Val Leu

830
CTT TCT CTC ACC GTC TTC CTG CTG CTC ATC ACC GAG ATC ATC CCG TCC ACC TCG CTG GTC
Leu Ser Leu Thr Val Phe Leu Leu Leu Ile Thr Glu Ile Ile Pro Ser Thr Ser Leu Val

850
ATC CCG CTC ATC GGC GAG TAC CTC CTC 930
Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Val

950
ATC ACG GTC TTC GTG CTC AAT GTG CAC CAC CGC TCG CCA CGC ACA CAC 1010
Ile Thr Val Phe Val Leu Asn Val His His Arg Ser Pro Arg Thr His Thr Met Pro Ala

1030
TGG GTG CGT AGA GTC TTC CTG GAC ATC GTG CCT CGC CTC CTC TTC ATG AAG CGC CCC TCT
Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg Leu Leu Phe Met Lys Arg Pro Ser

1070
GTG GTC AAA GAC AAC TGC CGG AGA CTT ATT GAG TCC ATG CAC AAG ATG GCC AAC GCC CCC
Val Val Lys Asp Asn Cys Arg Arg Leu Ile Glu Ser Met His Lys Met Ala Asn Ala Pro

1130
CGC TTC TGG CCA GAG CCT GTG GGC GAG CCC GGC ATC TTG AGT GAC ATC TGC AAC CAA GGT
Arg Phe Trp Pro Glu Pro Val Gly Glu Pro Gly Ile Leu Ser Asp Ile Cys Asn Gln Gly

1150
CTG TCA CCT GCC CCA ACT TTC TGC AAC CCC 1230
Leu Ser Pro Ala Pro Thr Phe Cys Asn Pro Thr Asp Thr Ala Val Glu Thr Gln Pro Thr

1250
TGC AAG TCA CCC CCC CTT GAG GTC CCT GAC TTG AAG ACA TCA GAG GTT GAG AAG GCC AGT
Cys Arg Ser Pro Pro Leu Glu Val Pro Asp Leu Lys Thr Ser Glu Val Glu Lys Ala Ser

1270
CCC TGT CCA TCG CCT GGC TCC TGT CCT CCA CCC AAG AGC AGC AGT GGG GCT CCA ATG CTC
Pro Cys Pro Ser Pro Gly Ser Cys Pro Pro Pro Lys Ser Ser Ser Gly Ala Pro Met Leu

1330
ATC AAA GCC AGG TCC CTG AGT GTC CAG CAT GTG CCC AGC TCC CAA GAA GCA GAA GAT
Ile Lys Ala Arg Ser Leu Ser Val Gln His Val Pro Ser Ser Gln Glu Ala Ala Glu Asp

1350
GGC ATC CGC TGC CGG TCT CGG AGT ATC CAG TAC TGT GTT TCC CAA GAT GGA GCT GCC TCC
Gly Ile Arg Cys Arg Ser Arg Ser Ile Gln Tyr Cys Val Ser Gln Asp Gly Ala Ala Ser

1430
CTG GCT GAC AGC AAG CCC ACC AGC TCC CCG ACC TCC CTG AAG GCC CGT CCA TCC CAG CTT
Leu Ala Asp Ser Lys Pro Thr Ser Ser Pro Thr Ser Leu Lys Ala Arg Pro Ser Gln Leu

1450
1510
1530
1550

FIG. 2B



1570 1590 1610
CCC GTG TCA GAC CAG GCC TCT CCA TGC AAA TGC ACA TGC AAG GAA CCA TCT CCT GTG TCC
Pro Val Ser Asp Gln Ala Ser Pro Cys Lys Cys Thr Cys Lys Glu Pro Ser Pro Val Ser

1630 1650 1670
CCA GTC ACT GTG CAC AAG GCG GGA GGC ACC AAA GCA CCT CCC CAA CAC CTG CCC CTG TCA
Pro Val Thr Val Leu Lys Ala Gly Gly Thr Lys Ala Pro Pro Gln His Leu Pro Leu Ser

1690 1710 1730
CCA GCC CTG ACA CGG GCA GTA GAA GGC GTC CAG TAC ATT GCA GAC CAC CTC AAG GCA GAA
Pro Ala Leu Thr Arg Ala Val Glu Gly Val Gln Tyr Ile Ala Asp His Leu Lys Ala Glu

1750 1770 1790
GAC ACT GAC TTC TCG GTG AAG GAG GAC TGG AAA TAC GTG GCC ATG GTC ATT GAC CGA ATC
Asp Thr Asp Phe Ser Val Lys Glu Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Ile

1810 1830 1850
TTC CTC TGG ATG TTC ATC ATT GTC TGC CTT CTG GGC ACT GTG GGA CTC TTC CTG CCT CCC
Phe Leu Trp Met Phe Ile Ile Val Cys Leu Lue Gly Thr Val Gly Leu Phe Leu Pro Pro

1870 1890 1917
TGG CTG GCT GCT TGC TGA TGGCTTCGACA GTGTTCTCAGGCTCACGTCTCCTGCTGACTTTGTTTCCCAG
Trp Leu Ala Ala Cys

1943 1969 1997
TTTCTTCTCCGACAAAGTTGGCCTCCCTTCATTTATTCCTGTTATTTTGGGCTTCGTGTTATTAATATCCTTCCCTGCC
TCTGTGGCGCATTGTAAGTTTTAAAAATTAATAGACCAAAGCC...3'

4-2 cDNA: 3' end

1867 1884 1912
CCC TGG CTG GCT GGT ATG ATC TAG GGAGCTGGTGGTGGCCAGCTCCACATCTCTGTAGGGCCATAC
Pro Trp Leu Ala Gly Met Ile

1937 1953 1991
GACTCGTCAGTCACCCACATCTTCCAAACCGGCTGACCATGAGACACCTAGGAGAGAGATGATGCTTCTTGGGAGATG

2016 2042 2070
GAAAGTTGGCCCTGCTTCTAGTCAGACTATGCGCGTGGTTGGAGAGAAATGAGGGCTGATACAGTTGCAGGCCGAGTCCC

2095 2121 2149
CATTAAAGTTTCTCCAGAGCAAGTGGCAGTACTCCCTGACTTACAGACAGCACACCCCATCTGTGTCAGAGAGAAATGA

2174 2200 2228
TCCCGAGTTGATCTCAGTTGTCTTTGAGGCCATGAAAAATTCATCCACCTTGAGGAACCCAGAGCCTCTCATGCTGTGG

2253 2279 2307
GATCAATAAGACCAAGAAATCTCCCACTGTGACTCTGCTGGCCACACCCCTCTCCCTCCCCAAGAAGTGGTCCCTCATCC
CCCAATTC...3'

FIG. 2C

[illegible]

FIG. 3A

Asp Phe Trp Glu Ser GAC TTC TGG GAA AGT	180 540	Glu Trp Val Ile Val Asp Ala Val Gly GAG TGG GTC ATC ATC GAT GCT GTG GGC	190 570	Tyr Asn Thr Arg Lys Tyr Glu Cys ACC TAC AAC ACC AGG AAG TAC GAG TGC TGT	200 600	Glu Ile Tyr Pro GAG ATC TAT CCT
Asp Ile Thr Tyr Ala GAC ATC ACC TAT GCC	210 630	Ile Ile Arg Arg Glu Pro Leu Phe Tyr ATC ATC CGA CGC CGC CTG CCG CTA TTC TAC	220 660	Ile Asn Leu Ile Ile Pro Cys Leu ATC AAC CTC ATC ATC CCG TGC CTG CTC	230 690	Ser Cys Leu Thr TCC TGT CTC ACC
Val Leu Val Phe Tyr GTG CTG GAC TTC TAT	240 720	Pro Ser Glu Cys Gly Glu Lys Val Thr CTG CCT TCA GAG TGT GGC GAG AAG GTC ACA	250 750	Cys Ile Ser Val Leu Leu Ser Leu Thr CTG ATC TCG GTG CTG CTT TCT CTC ACC	260 780	Phe Leu Leu Leu TTC CTG CTG CTC
Ile Thr Glu Ile Ile ATC ACC GAG ATC ATC	270 810	Ser Thr Ser Leu Val Ile Pro Leu Ile CCG TCC ACC TCG CTG GTC ATC CCG CTC ATC	280 840	Glu Tyr Leu Leu Phe Thr Met Ile Phe GAG TAC CTC CTC TTC ACC ATG ATC TTC	290 870	Thr Leu Ser Ile ACC CTC TCC ATC
Val Ile Thr Val Phe GTG ATC ACC GTC TTC	300 900	Leu Asn Val His His Arg Ser Pro Arg CTC AAT GTG CAC CAC CGC TCG CCA CGC	310 930	His Thr Met Pro Ala Trp Val Arg Arg CAC ACG ATG CCC GCC TGG GTG CGT AGA	320 960	Phe Leu Asp Ile TTC CTG GAC ATC
Val Pro Arg Leu Leu GTG CCT CGC CTC CTC	330 990	Met Lys Arg Pro Ser Val Val Lys Asp ATG AAG CGC CCC TCT GTG GTC ANA GAC	340 1020	Cys Arg Arg Leu Ile Glu Ser Met His TGC CGG AGA CTT ATT GAG TCC ATG CAC	350 1050	Met Ala Asn Ala ATG GCC AAC GCC
Pro Arg Phe Trp Pro CCC CGC TTC TGG CCA	360 1080	Pro Val Gly Glu Pro Gly Ile Leu Ser CCT GTG GGC GAG CCC GGC ATC TTG AGT	370 1110	Ile Cys Asn Gln Gly Leu Ser Pro Ala ATC TGC AAC CAA GGT CTG TCA CCT GCC	380 1140	Thr Phe Cys Asn ACT TTC TGC AAC
Pro Thr Asp Thr Ala CCC ACC GAC ACA GCA	390 1170	Glu Thr Gln Pro Thr Cys Arg Ser Pro GAG ACC CAG CCT ACG TGC AGG TCA CCC	400 1200	Leu Glu Val Pro Asp Leu Lys Thr CTT GAG GTC CCT GAC TTG AAG ACA TCA	410 1230	Val Glu Lys Ala GTT GAG AAG GCC

FIG. 3B

Ser Pro Cys Pro Ser Pro Gly Ser Cys Pro Pro Pro Lys Ser Ser Ser 430
 AGT CCC TGT CCA TCG CCT GGC TCC TGT CCT CCA CCC CAG AGC AGT 1290
 His Val Pro Ser Ser Glu Ala Ala Glu Asp Gly Ile Arg Cys Arg 460
 CAT GTG CCC AGC TCC CAA GAA GCA GCA GAA GAT GGC ATC CCG TGC 1380
 Ser Leu Ala Asp Ser Lys Pro Thr Ser Ser Pro Thr Ser Leu Lys Ala 490
 TCC CTG GCT GAC AGC AAG CCC ACC AGC TCC CCG ACC TCC CTG AAG 1470
 Lys Cys Thr Cys Lys Glu CCA TCT CCT CCT GTG TCC CCA GTC ACT Thr Val Leu 520
 AAA TGC ACA TGC AAG GAA GAA GAA GAA GAA GAA GAA GAA GAA GAA 1560
 Ser Pro Ala Leu Thr Arg Ala Val Glu Gly Val Glu Tyr Ile Ala Asp 550
 TCA CCA GCC CTG ACA CCG GCA GTA GAA GAA GGC GTC CAG TAC ATT GCA 1650
 Trp Lys Tyr Val Ala Met Val Ile Asp Arg Ile Phe Leu Trp Met Phe 580
 TGG AAA TAC GTG GCC ATG ATG GTC ATT GAC CGA ATC TTC CTC TGC ATG 1740
 Pro Trp Leu Ala Gly Met Ile 600
 CCC TGG CTG GCT GGT ATG ATC TAG GGACGTGGTGGTGCCAGCTCCACATCTCTGTAGGCCCATACGACTGCTCAGTCCACCCACATCTCCAAACGGCTGACCATGAG 1860
 ACACCCTAGGAGAGATGATGCTTCTTGGGAGATGGAAAGTTGGCCCTGGTTCTAGTCAGACTATGGCGTGGTTGGAGAGAAATGACGGGCTGATACAGTTGCAGGCCGAGTCCCCCAT 1920
 1980
 2010

FIG. 3C

FIG. 4A



ALPHA4 F V L N V H Y R S P R T H T M P A W V R R V F L D I V
ALPHA3 F V L N V H Y R T P T T H T M P T W V K A V F L N L L
ALPHA1 I V I N T H Y R S P S T H I M P E W V R K V F I D T I
----->

ALPHA4 P R L L F - - - M K R P S V V K D N C R R L I E S M H
ALPHA3 P R V M F - - - M T R P T S G E G D T P K T - - - -
ALPHA1 P N I M F F S T M K R P S R D K Q E K R I F - - - -

ALPHA4 X M A N A P R F W P E P V G E P G I L S D I C H Q G L
ALPHA3 - - - - - - - - - - R T F Y G A E L S N L N C F S R
ALPHA1 - - - - - - - - - - T E D I D I S D I S G X P G

ALPHA4 S P A P T F C N P T D T A V E T Q P T C R S P P L E V
ALPHA3 A D S K S C K E G Y P C O D G T C C Y C H H R R V K I
ALPHA1 P P P M G F H - - - - - - - - - - - - - - - - - - -

ALPHA4 P D L K T S E V E K A S P C P S P G S C P P P K S S S
ALPHA3 S N F - - - - - - - - - - - - - - - - - - - S A N L T R S S S
ALPHA1 -

ALPHA4 G A P M L I K A R S L S V Q W V P S S Q E A A E D G I
ALPHA3 S E S V -
ALPHA1 -

ALPHA4 R C R S R S I O Y C V S Q D G A A S L A D S K P T S S
ALPHA3 -
ALPHA1 -

ALPHA4 P T S L X A R P S Q L P V S D Q A S P C X C T C K E P
ALPHA3 -
ALPHA1 -

ALPHA4 S P V S P V T V L X A G G T X A P P Q H L P L S P A L
ALPHA3 -
ALPHA1 -
-----<

ALPHA4 T R A V E G V O Y I A D H L K A E D T D F S V K E D W
ALPHA3 K E A I O S V K Y I A E N M K A Q N V A K E I O D D W
ALPHA1 K S A I E G V K Y I A E T M K S D Q E S N N A A E E W
----->
alpha helix

ALPHA4 K Y V A M V I D R I F L W M F I I V C L L G T V G L F
ALPHA3 X Y V A M V I D R I F L W V F I L V C I L G T A G L F
ALPHA1 K Y V A M V M D H I L L G V F M L V C L I G T L A V F
-----< MSR IV

ALPHA4 L P P W L A G M I
ALPHA3 L O P L M A - R D D T
ALPHA1 A G R L I E L H Q Q G
----->

FIG. 4B

FIG. 5A

Clone 4-1;
Antisense

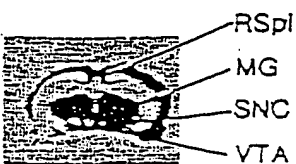
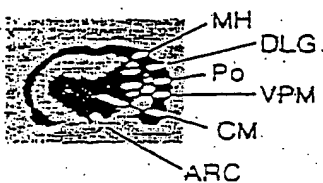
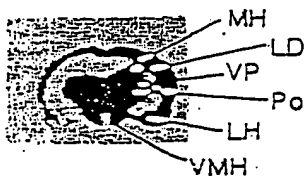
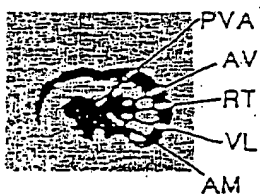


FIG. 5B

Clone 4-1;
Sense

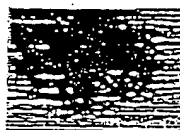
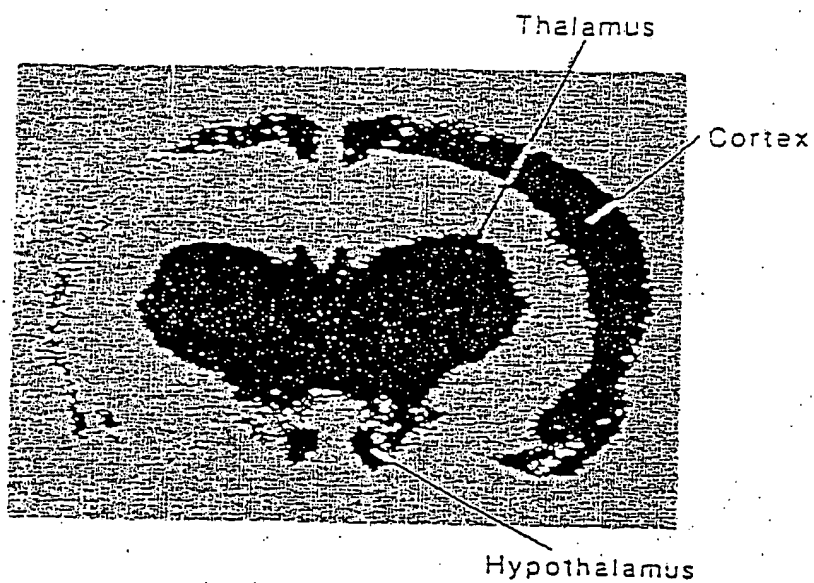
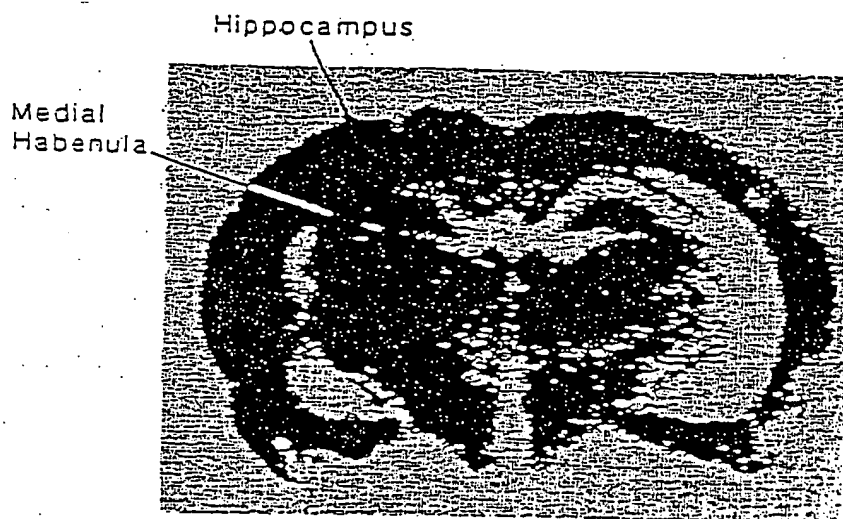


FIG. 6A



PROBE: Alpha 4

FIG. 6B



PROBE: Alpha 3

FIG. 7A

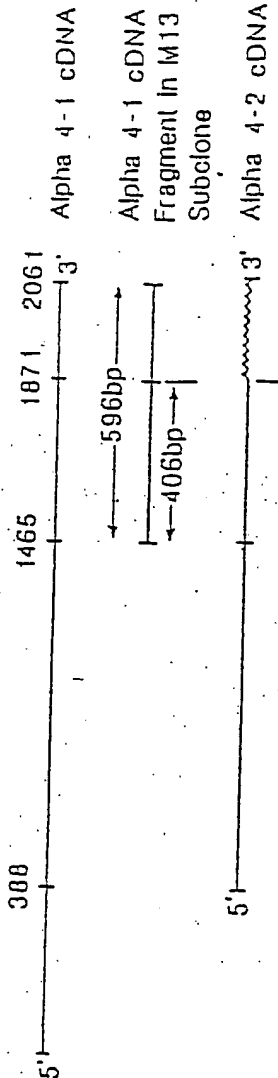


FIG. 7B

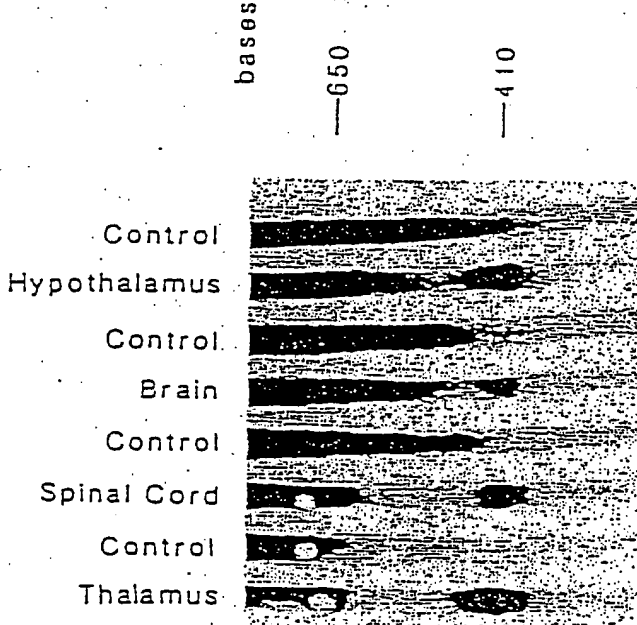
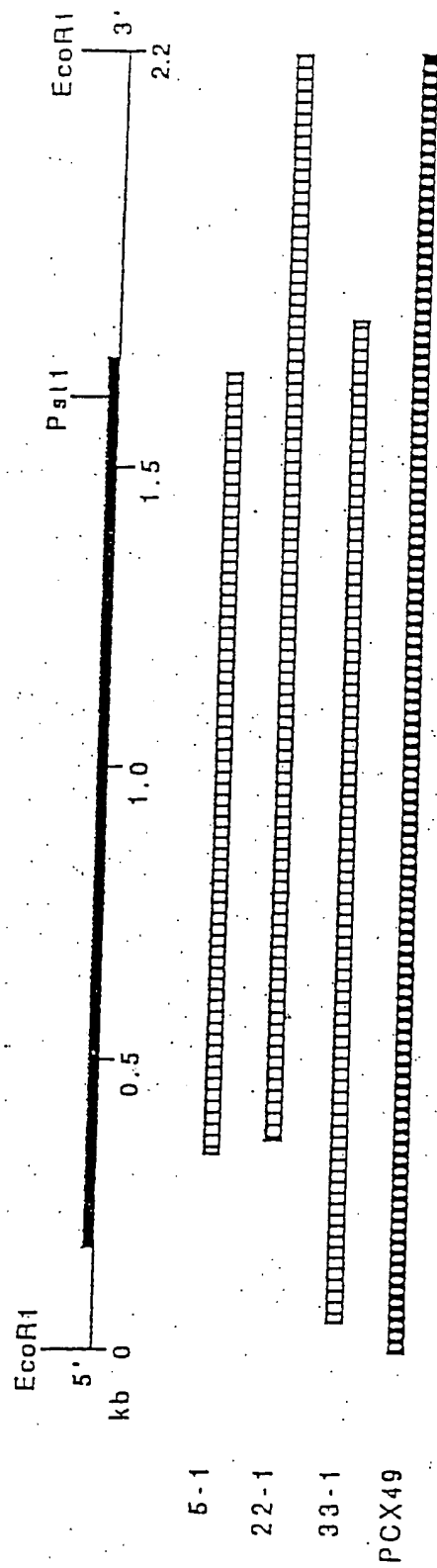


FIG. 8





5'.....-179 GGGGACACACACCGGGGACCGGCAAGAGCCGGGACCTCCCTCGTTGACAGGAACCTGCCCGTTTCAGTGAGCACCTTTAGACC-100
TGGAGGGCCGCGAGCCACCCCGGGAGCAGGGGCTGCGGGCTTCAGCACACCGGACGCGCTCGACCCCGCAGCCCTAGTATCCGAGAGGCTGCGCGGCT-1
ATG CTG GCT TGC ATG GCC GGG CAC TCC AAC TCA ATG GCG CTG TTC AGC TTC AGC CTT CTT TGG CTG TGC TCA GGG
Met Leu Ala Cys Met Ala Gly His Ser Asn Ser Met Ala Leu Phe Ser Phe Ser Leu Leu Trp Leu Cys Ser Gly
1
GTT TTG GGA ACT GAC ACA GAG GAG GAG CTA GTG GAG CAT CTC TTA GAT CCC TCC CGC TAT AAC AAG CTG ATT CGT
Val Leu Gly Thr Asp Thr Glu Glu Arg Leu Val Glu His Leu Leu Asp Pro Ser Arg Tyr Asn Lys Leu Ile Arg
26
CCA GCT ACT AAC GGC ICT GAG CTG GTG ACT GTA CAG CTC ATG GTA TCA TTG GCT CAG CTC ATT AGT GTG CAC GAG
Pro Ala Thr Asn Gly Ser Glu Leu Val Thr Val Gln Leu Met Val Ser Leu Ala Gln Leu Ile Ser Val His Glu
51
CGG GAG CAG ATC ATG ACC ACC AAT GTC TGG CTG ACC CAG GAG TGG GAA GAT TAC CGC CTC ACA TGG AAG CCT GAG
Arg Glu Gln Ile Met Thr Thr Thr Asn Val Trp Leu Thr Gln Glu Trp Glu Asp Tyr Arg Leu Thr Trp Lys Pro Glu
76
GAC TTC GAC AAT ATG AAG AAA GTC CGG CTC CCT TCC AAA CAC ATC TGG CTC CCA GAT GTG GTT CTA TAC AAC AAT
Asp Phe Asp Asn Met Lys Lys Val Arg Leu Pro Ser Lys His Ile Trp Leu Pro Asp Val Val Leu Tyr Asn Asn
101
GCT GAC GGC ATG TAC GAA GTC TCC TTC TAT TCC AAT GCT GTG GTC TCC TAT GAT GGC AGC ATC TTT TGG CTA CCA
Ala Asp Gly Met Tyr Glu Val Ser Phe Tyr Ser Asn Ala Val Val Ser Tyr Asp Gly Ser Ile Phe Trp Leu Pro
126
CCT GCC ATC TAC AAG AGT GCA TGC AAG ATT GAG GTG AAG CAC TTC CCA TTT GAC CAG AAT TGC ACC ATG AAG
Pro Ala Ile Tyr Lys Ser Ala Cys Lys Ile Glu Val Lys His Phe Pro Phe Asp Gln Gln Asn Cys Thr Met Lys
151

FIG. 9A

540
 TTT CGC TCA TGG ACC TAC GAC CGT ACT GAG ATT GAC CTG GTG CTC AAA AGT GAT GTG GCC AGT CTG GAT GAC TTC 600
 Phe Arg Ser Trp Thr Thr Tyr Asp Arg Thr Glu Ile Asp Leu Val Leu Lys Ser Asp Val Ala Ser Leu Asp Phe
 176
 ACA CCC AGC GGG GAG TGG GAC ATC ATC GCA CTG CCA GGC CGA CGC AAC GAG AAC CCA GAC GAC TCC ACC TAT GTG
 Thr Pro Ser Gly Glu Thr Ile Ile Ala Leu Pro Gly Arg Arg Arg Asn Glu Asn Pro Asp Ser Thr Tyr Val
 201
 630
 GAC ATC ACC TAT GAC TTT ATC ATT CGT CGC AAA CCA CTC TTC TAC ACT ATC AAC CTC ATC CCC TGC GTA CTC 750
 Asp Ile Thr Tyr Asp Phe Ile Ile Arg Arg Arg Lys Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile Pro Cys Val Leu
 226
 690
 ATC ACC TCG CTG GCC ATC CTG GTC TTC TAC CTG CCC TCA GAC TGT GGT GAA AAG ATG ACA CTT TGT ATT TCT GTG
 Ile Thr Ser Leu Ala Ile Leu Val Phe Tyr Tyr Leu Pro Ser Asp Cys Gly Glu Lys Met Thr Thr Leu Cys Ile Ser Val
 251
 780
 CTG CTA GCA CTC ACG GTG TTC CTG CTC ATC TCC AAG ATT GTG CCT CCC ACC TCC CTC GAT GTA CCG CTG CTC GTG 900
 Leu Leu Ala Leu Thr Thr Val Val Phe Leu Leu Leu Ile Ser Lys Ile Val Val Pro Thr Ser Leu Asp Val Pro Leu Val
 276
 840
 GGC AAG TAC CTC ATG TTT ACC ATG GTG CTA GTC ACC TTC TCC ATC GTC ACC AGC GTG TGT GTG CTC AAT GTG CAC
 Gly Lys Tyr Leu Met Phe Thr Thr Met Val Leu Val Thr Ser Ile Val Thr Ser Val Cys Val Leu Asn Val His
 301
 930
 CAC CGC TCG CCT ACC ACG CAC ACC ATG GCC CCC TGG GTC AAG GTG GTC TTC CTG GAG AAG CTG CCC ACC CTG CTC 1050
 His Arg Ser Pro Thr Thr Thr His Thr Met Ala Pro Trp Val Lys Val Val Phe Leu Glu Lys Leu Pro Thr Leu Leu
 326
 990
 TTC CTG CAG CAG CCA CGC CAC CGC TGT GCA CGT CAG CGT CTG CGC TTG AGG AGG CGC CAG CGA GAG CGT GAG GGC
 Phe Leu Gln Gln Pro Arg Arg His Arg Cys Ala Arg Gln Arg Leu Arg Arg Arg Gln Arg Glu Arg Glu Gly
 351
 1080
 1110

FIG. 9B



1140 GAG GCG GTT TTC TTC CGT GAA GGT CCT GCG GCT GAC CCA TGT ACC TGC TTT GTG AAC CCT GCA TCA GTG CAG GGC 1200
Glu Ala Val Phe Phe Arg Glu Gly Pro Ala Ala Asp Pro Cys Thr Cys Phe Val Asn Pro Ala Ser Val Gln Gly
376

1230 TTG GCT GGG GCT TTC CGA GCT GAG CCC ACT GCA GCC GGC CCG GGG GGT TCT GTG GGG CCA TGC AGC TGT GGC CTC 1260
Leu Ala Gly Ala Phe Arg Ala Glu Pro Thr Ala Ala Gly Pro Gly Arg Ser Val Gly Pro Cys Ser Cys Gly Leu
401

1290 CCG GAA GCA GTG GAT GGC GTA CGC TTC ATT GCG GAC CAC ATG CGA AGT GAG GAT GAT GAC CAG AGT GTG AGG GAG 1350
Arg Glu Ala Val Asp Glu Val Arg Phe Ile Ala Asp His Met Arg Ser Glu Asp Asp Asp Gln Ser Val Arg Glu
426

1380 GAC TGG AAA TAC GTT GCC ATG GTG ATC GAC CGC CTG TTC CTG TGG ATC TTT GTG TTT GTG TTT GGC ACC 1410
Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Leu Phe Leu Trp Ile Phe Val Phe Val Cys Val Phe Gly Thr
451

1440 GTC GGC ATG TTC CTG CAG CCT CTC TTC CAG AAC TAC ACT GCC ACT ACC TTC CTC CAC CCT GAC CAC TCA GCT CCC 1500
Val Gly Met Phe Leu Gln Pro Leu Phe Gln Asn Tyr Thr Ala Thr Thr Phe Leu His Pro Asp His Ser Ala Pro
476

AGC TCC AAG TGAGGTCTCATTCATTGTCAGCTCCTCACCCCGTGACCCCTGCGGTTTCAGTACTGGGTGCAAGATGGATCTCTCCCCACTCCACTGA 1596
Ser Ser Lys

AGCCTGCTTACACACCTCCGTTACACATAGTCTCCAGCCCTGGAGGCTGGACCCGCTGCCCTTGTGGTCGAGCCCTTCTCCCTCTGAGCTCGTTCA 1695
GGCAGGAGTGCCATGTTGGGGGCCACGGCTGGTAAGTAGAGGCCAGAGATCACAGAGCCACCTACCCCGATGAGGTGCTGGAGAGGCGCCAAAGAAAG 1794
AGACAGAGTTATCTGTGACCTCCAAAGTCATCGGAGAGGAGGAGTAGGATAAGGGGCTCAGACTCTGGCAGAGTGGCGCTAGTACTTGGCGGCCACCCCA 1893
CTTAAGTGAGCGACACTGGTCTGGGAGGACTCGAAGTGTGGGAGCTCTCTTGGGAGCTCGGTCTCCACCCTGTACCTCAGAGGGGCTCCAGACCCCGG 1992
GCTTCAGGTTCCCTTCTGCCAGTGC.....3'

FIG. 9C

NEUROIAL AND MUSCLE NICOTINIC ACETYLCHOLINE RECEPTOR SUBUNITS

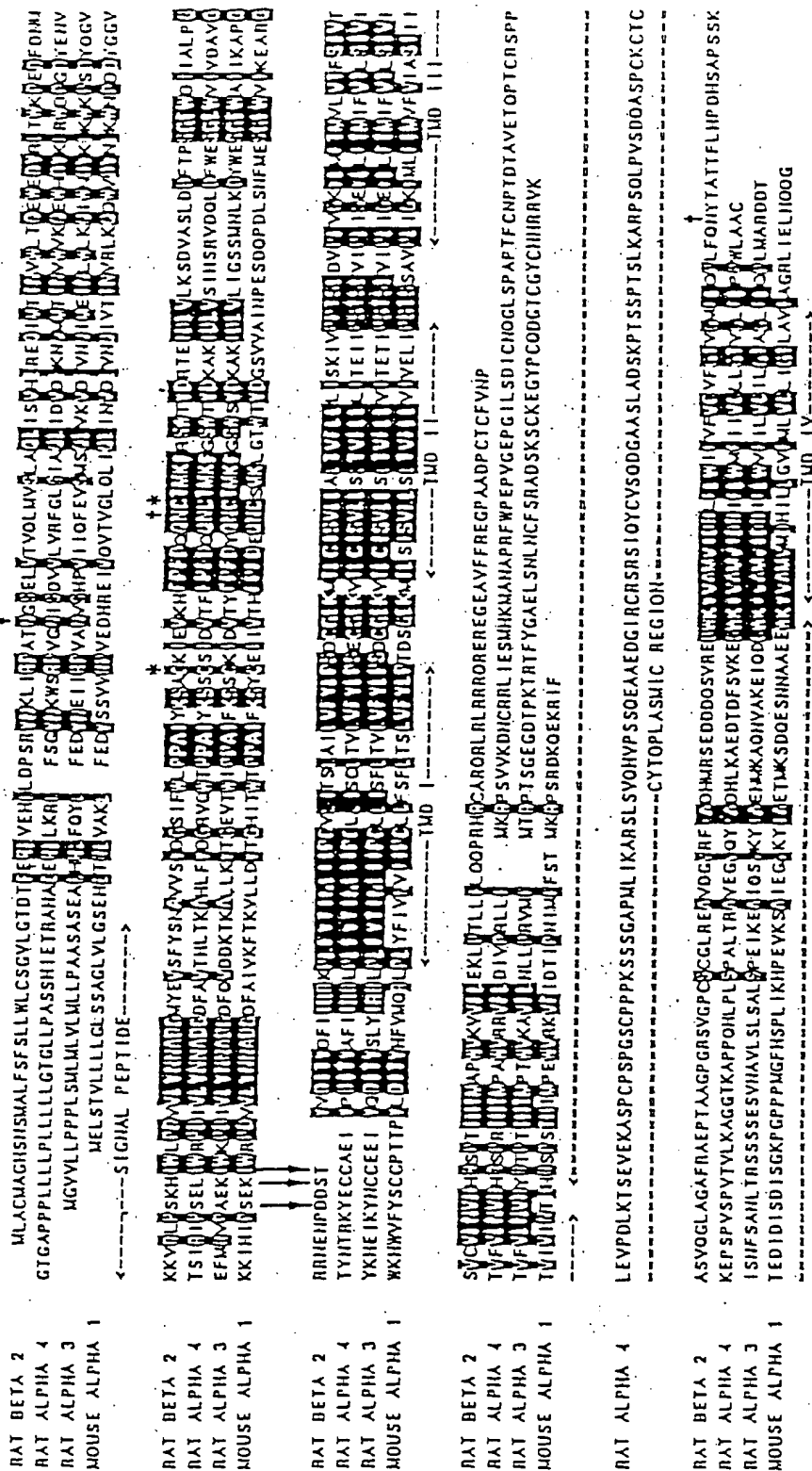
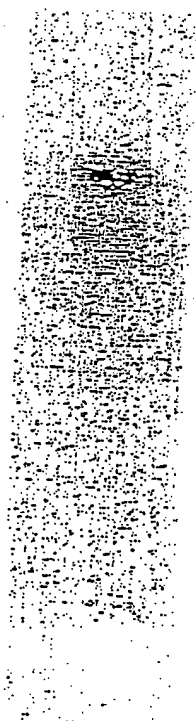


FIG. 10

FIG. 11A

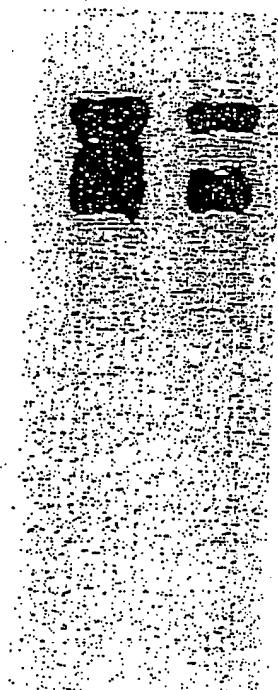


—28S

—18S

FIG. 11B

1 2



28S—

18S—

FIG. 12A

ANTISENSE

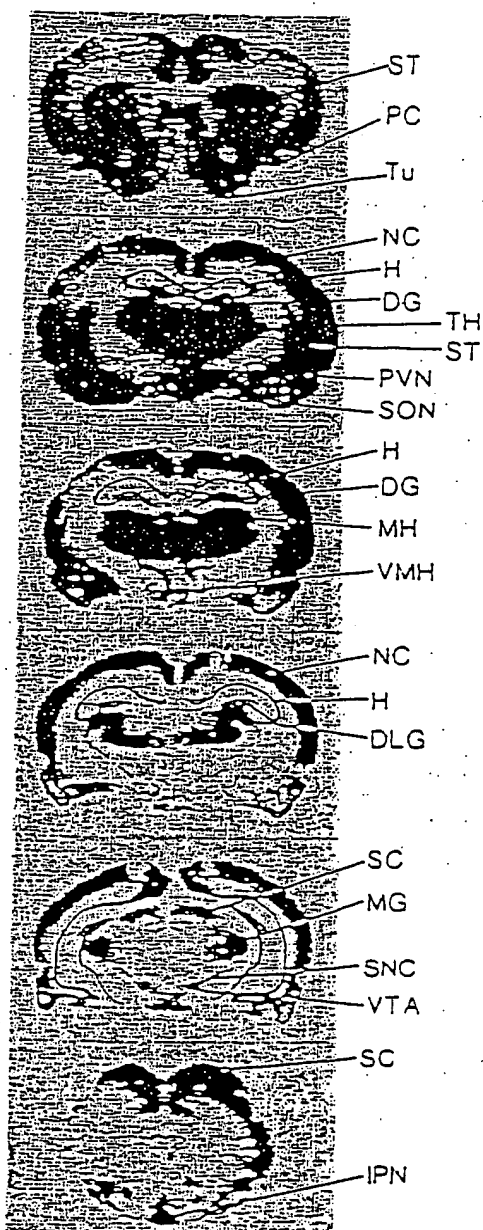


FIG. 12B

SENSE



[illegible]

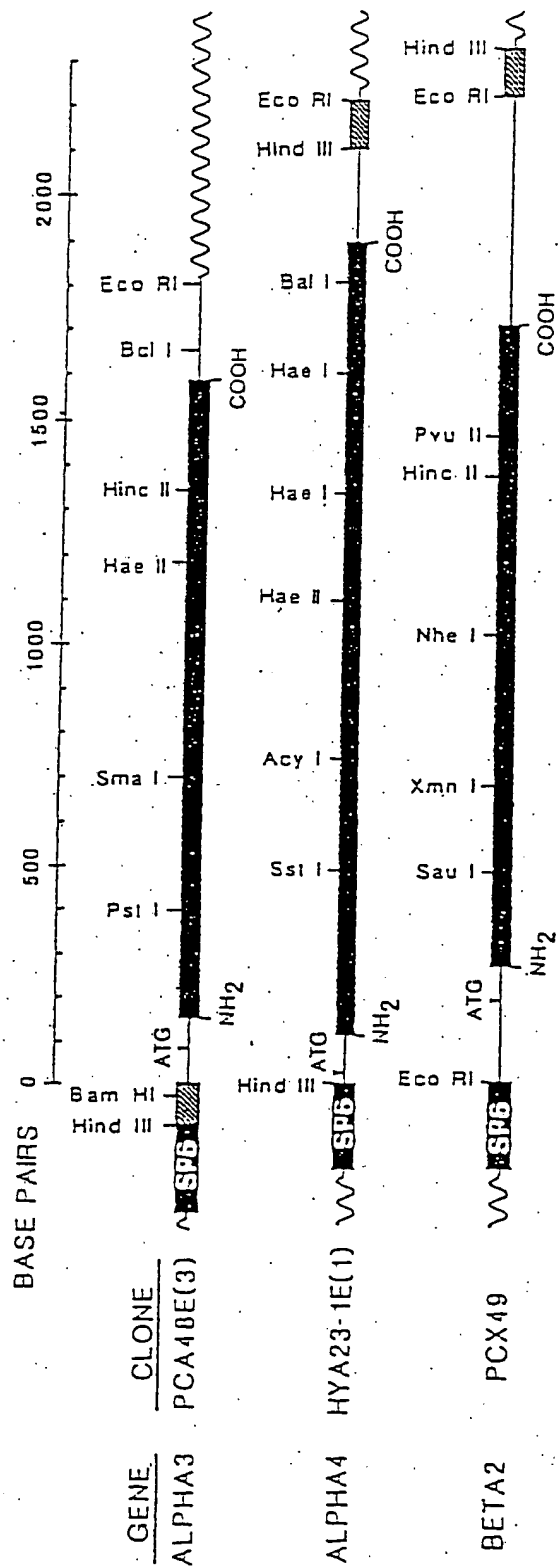


FIG. 14

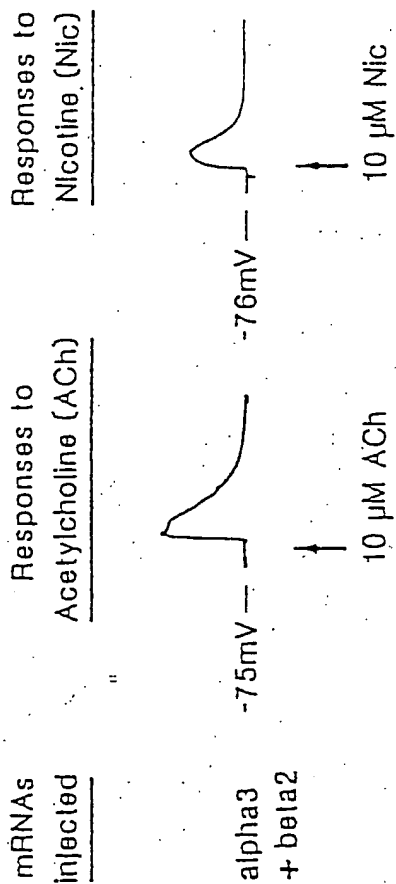


FIG. 15A

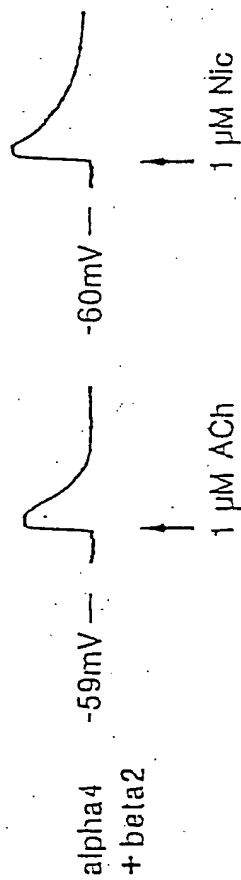


FIG. 15B

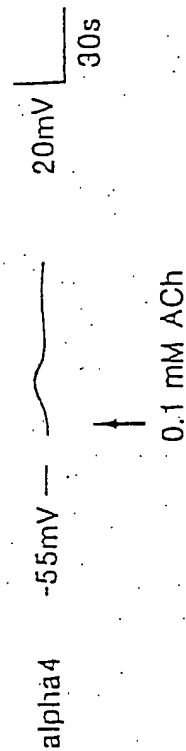


FIG. 15C

FIG. 16A

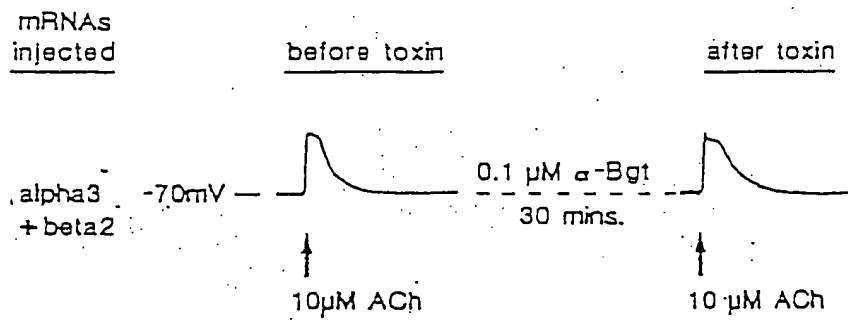


FIG. 16B

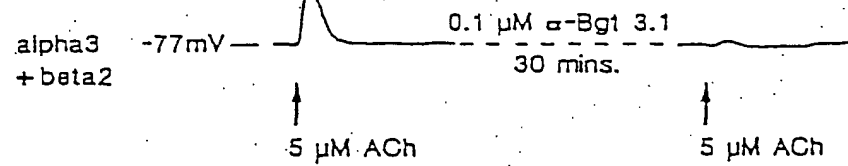


FIG. 16C

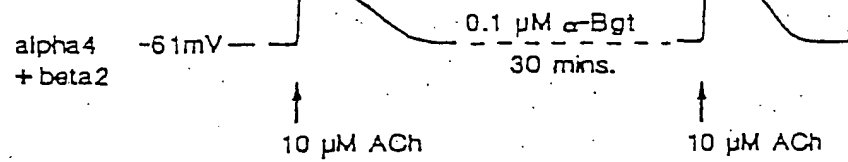
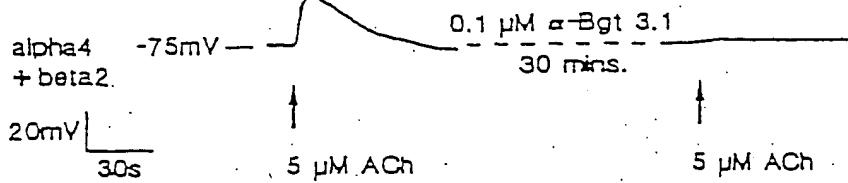


FIG. 16D



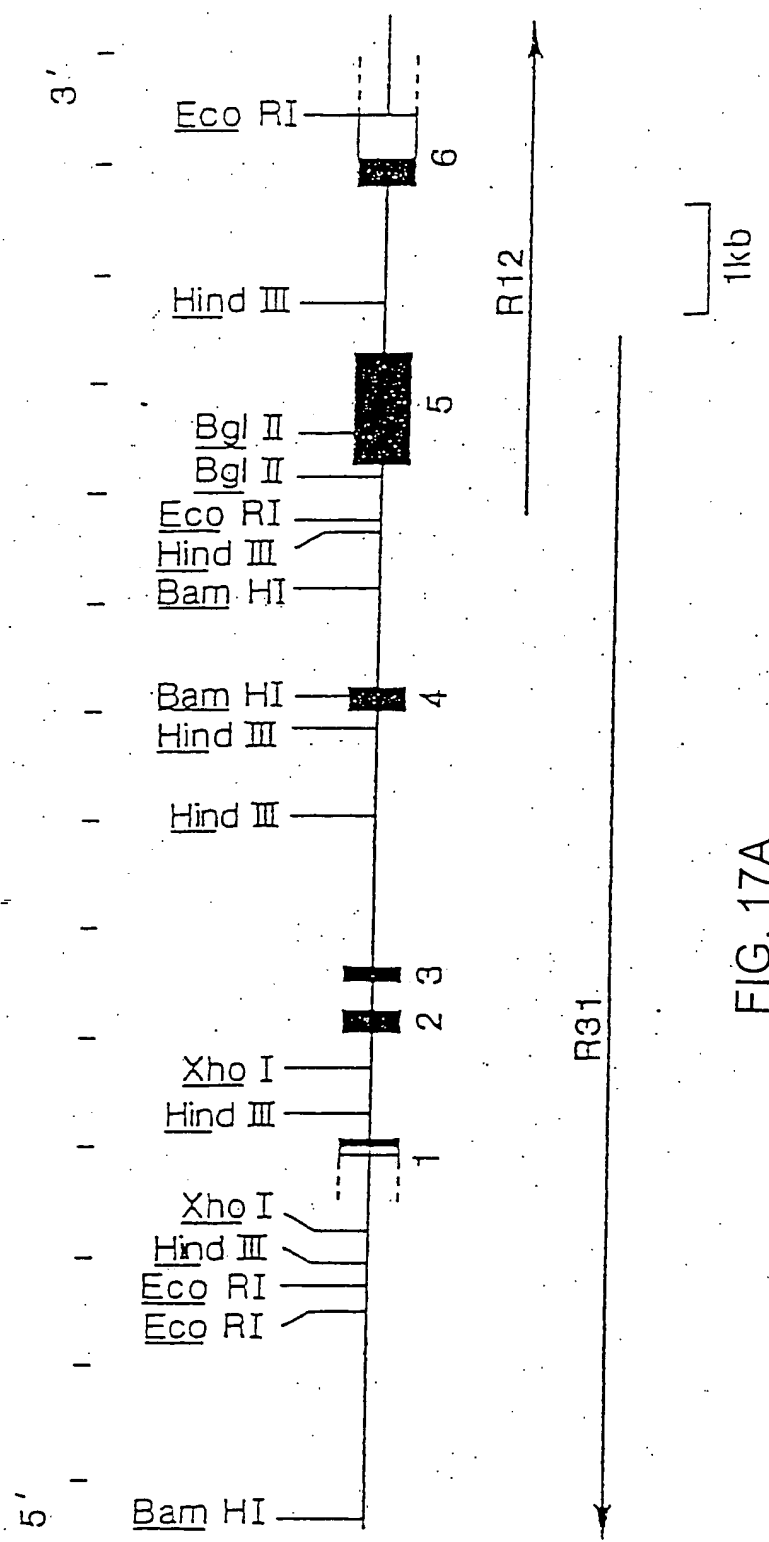


FIG. 17A

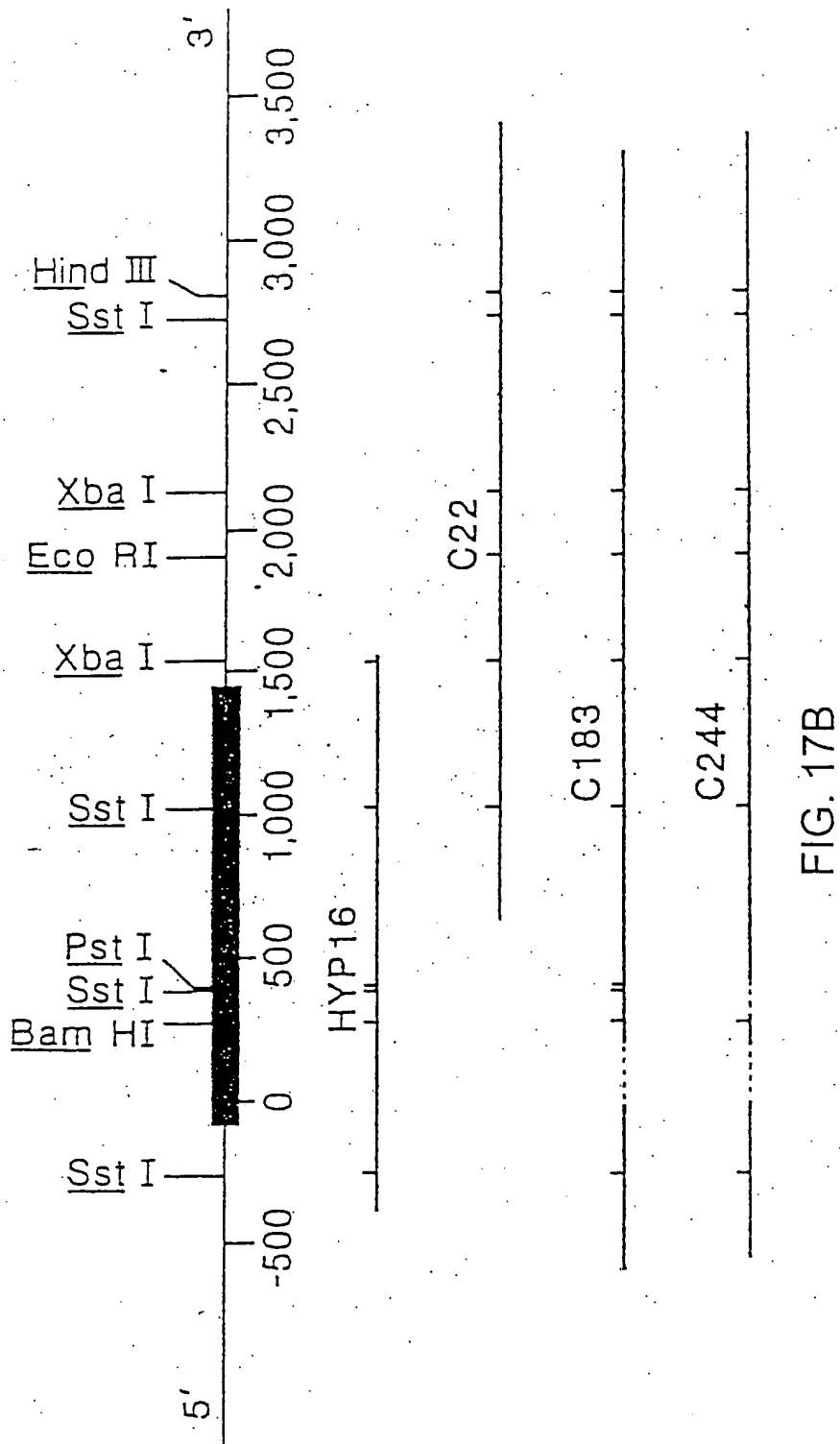


FIG. 17B

5'ACTGAGCATTC
 -360
 TGTGAACCTCGGATCACCTATCTCCAGGAGCTAGCTGATCCCTCATCCCAACAGTGCCCTCCCAACCTTGCGAGTTCTGTGCTGGGCAACCATGAGCTGAGCTCTG
 -270
 TTCTGCACCTGTGCTCTCCAGGAGCCCTCGTCAGCCACCCAGGCTCCAGCGGTTGGTTCTCTGCATCCCTTGAGGGGCTGTCTTCTATGACAATTGCAGAGAGACAGT
 -150
 GCCTCAAGAGAGCCAGCTCTTGGTAGTCCAGGGAACCCCTCTGAAGCC ATG ACC CTT TCC CAT TCT GCT CTC CAG TTC TGG ACA CAT CTT TAT CTC
 -60
 Met Thr Leu Ser His Ser Ala Leu Gln Phe Thr Trp His Leu Tyr Leu
 -120
 TGG TGT CTC CTT CTG GTC CCA G G gtgagt.....tatccccacag TG TTG ACC CAG CAA GGC TCA CAC ACC CAT GCT GAG GAC CGC CTG TTC
 -30
 Trp Cys Leu Leu Val Pro Ala V al Leu Thr Gln Gln Gly Ser His Thr His Ala Glu Asp Arg Leu Phe
 -10
 AAA CAC CTG TTT GGA GGC TAC AAT CGC TGG GCA CGG CCA GTG CCC AAC ACT TCT GAT GTG GTC ATC GTG CGC TTT GGA TTA TCC ATT GCT
 60
 Lys His Leu Phe Gly Gly Tyr Asn Arg Trp Ala Arg Pro Val Pro Asn Thr Ser Asp Val Ile Val Arg Phe Gly Leu Ser Ile Ala
 20
 CAG CTC ATA GAT GTG gtgggc.....gctacaacag CAT GAG AAG AAT CAA ATG ATG ACC AAT GTC TGG CTA AAG CAG gtaaac.....
 150
 Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met Thr Thr Asn Val Trp Leu Lys Gln
 50
ccctaagcag GAA TGG AAT GAC TAC AAG CTG CGC TGG GAC CCG GCT GAG TTT GGC AAT GTC ACC TCC CTG CGC GTC CCT TCA GAG ATG
 210
 Glu Trp Asn Asp Tyr Lys Leu Arg Trp Asp Pro Ala Glu Phe Gly Asn Val Thr Ser Leu Arg Val Pro Ser Glu Met
 70
 80

FIG. 18A

270 ATC TGG ATC CCA GAC ATT GTC CTC TAC AAC AA gtaaga.....ctcttccag T 300
 ile Trp Ile Pro Asp Ile Val Val Leu Tyr Asn As 100
 90
 GCT CAC CTC TTC TTC ACG GGC ACT GTG CAC TGG GTG CCC CCA GCC ATC TAC 360
 Ala His Leu Phe Phe Thr Gly Thr Val His Trp Val Pro Pro Ala Ile Tyr 120
 360
 GAC CAG CAG AAC TGC AAG ATG AAG TTT GGC TCC TGG ACA TAT GAC AAG GCC 480
 Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser Trp Thr Tyr Asp Lys Ala 160
 480
 AAG GAC TAC TGG GAG AGT GGC GAG TGG GCC ATT ATC AAT GCC ACC GGA ACC 540
 Lys Asp Tyr Trp Glu Ser Gly Glu Trp Ala Ile Ile Asn Ala Thr Gly Thr 180
 540
 CCC GAT GTC ACC TAC TTT TAC Tyr Tyr Phe Val Ile Arg Arg Leu Pro Leu Phe Tyr Thr 630
 Pro Asp Val Thr Tyr Tyr Phe Val Ile Arg Arg Leu Pro Leu Phe Tyr Thr 210
 630
 ACT GTG CTC GTG TTC TAC CTC CCT TCC GAG TGT GGA GAG AAG ATC ACG CTG 720
 Thr Val Leu Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Ile Thr Leu 240
 720
 CTC ATC ACG GAG ATC ATC CCG TCC ACC TCG CTG GTC ATC CCA CTC ATC GGC 810
 Leu Ile Thr Glu Ile Ile Pro Pro Ser Thr Ser Leu Val Ile Pro Leu Ile Gly 270
 810
 330 GCA GAT GGG GAG TTT GCG GTG ACC CAC ATG Met 110
 n Ala Asp Gly Glu Phe Ala Val Thr His 100
 330
 420 AGC TCC TGC AGC ATC GAT GTG ACC TTC Phe 140
 Lys Ser Ser Cys Ser Ile Asp Val Thr Phe 140
 420
 510 GAT CTG GAG CAG ATG GAG AGG ACA GTG 170
 Ile Asp Leu Glu Gln Met Glu Arg Thr Val 170
 510
 600 AAC AGT AAG AAG TAC GAC TGC TGC GCG GAG 200
 Tyr Asn Ser Lys Lys Tyr Asp Cys Cys Ala 200
 600
 690 AAC CTC ATC ATC CCA TGC CTG CTC ATC TCC 230
 Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile 230
 690
 780 ATC TCG GTG CTG CTA TCT CTC ACT GTC 260
 TCC Cys Ile Ser Val Leu Leu Ser Leu Thr Val 260
 780
 870 TAC CTG CTC TTC ACC ATG ATC TTT GTC 290
 TAC Tyr Leu Leu Phe Thr Met Ile Phe Val 290
 870

FIG. 18B



ATC GTT ATC ACA GTC TTC GTG 900 AAT GTA CAC CAC CGC TCC CCC AGC ACC 930 AAC ATG CCC AAC TGG GTA AGG GTA GCC CTA GGC
11e Val 11e Thr Val Phe Val 300 Leu Asn Val 11s 11s Arg Ser Pro Ser Thr 310 His Asn Met Pro Asn Trp Val Arg Val Ala 320 Leu Leu Gly

CGG GTG CCC AGG TGG CTG ATG 990 AAC CGG CCC CTG CCA CCT ATG GAG CTC CAT 1020 GCC TCC CCG GAT CTG AAG CTC AGC CCC TCA TAC CAT
Arg Val Pro Arg Trp Leu Met 330 Met Asn Arg Pro Leu Pro Pro Met Glu Leu 340 His Glu Ser Pro Asp Leu Lys Leu Ser Pro 350 Ser Tyr 11s

TGG CTA GAG ACT AAC ATG GAT 1080 GGA GAA AGG GAG GAG ACA GAG GAA GAG GAA GAA GAT GAA AAC ATA TGT GTG TGT GCA GGC
Trp Leu Glu Thr Asn Met Asp 360 Ala Gly Glu Arg Glu Glu Thr Glu Glu Glu Glu Asp Glu Asn 11e Cys Val Cys Ala Gly 380

CTT CCA GAC TCT TCG ATG GGT 1170 CTC TAT GGC CAT GGC GGC CTG CAT CTG AGA GCC ATG GAG CCT GAG ACC AAG ACT CCA TCC CAG GCT
Leu Pro Asp Ser Ser Met Gly 390 Leu Tyr Gly 11s Gly Gly Leu His Leu Arg 400 Ala Met Glu Pro Glu Thr Lys Thr Pro Ser Glu Ala

AGC GAG ATT CTG CTG TCA CCT 1260 ATA CAG AAA GCA CTA GAA GGT GTA CAC TAC ATT GCT GAC CGT CTG AGG TCT GAG GAT GCT GAC TCT
Ser Glu 11e Leu Leu Ser Pro 420 Gln 11e Gln Lys Ala Leu Glu Gly Val His 430 Tyr 11e Ala Asp Arg Leu Arg Ser Glu Asp Ala Asp Ser 440

TCG gtgaagt.....ctaacttcag 1350 GTG AAG GAA GAC TGG AAG TAT GTG GCC ATG GTG GTA GAC CGG ATA TTC CTC TGG CTG TTC ATT ATC
Ser Val Lys Glu Asp Trp Lys Tyr Val Ala Met Val Val Asp Arg 11e Phe 460

GTC TCG TTC CTG GGG ACC ATC GGA CTC TTC CTT CCT CCA TTC CTG GCT GGA ATG ATC TAA CTTCATGTCCTTCATGTTGGCTCCMAGGTGGCCTTCGTA
Val Cys Phe Leu Gly Thr 11e Gly Leu Phe Leu Pro Pro Phe Leu Ala Gly Met 11e 470
1410 1440 1470

1500 ACTATCTCTAGTCTCTGTGMAATGGAGCCATCTCTAGMTACTCTTTTGAC.....3'

FIG. 18C

FIG. 20A

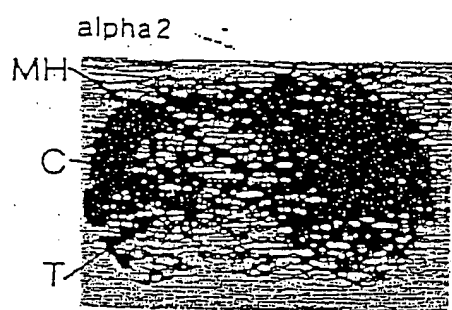
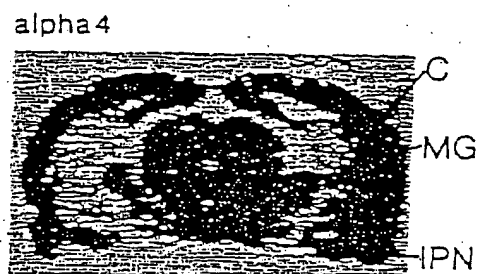
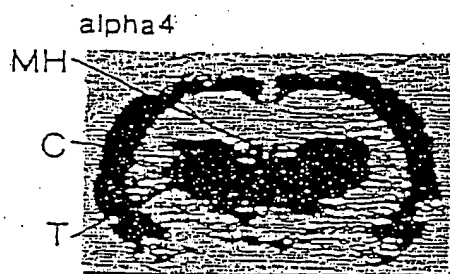
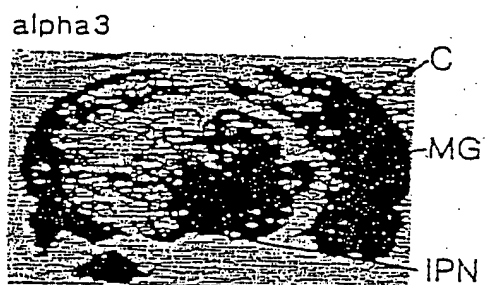
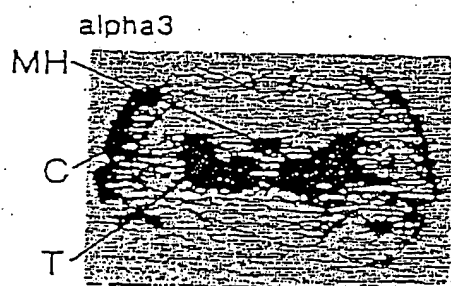
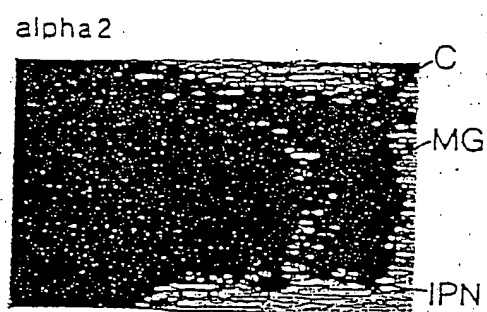


FIG. 20B



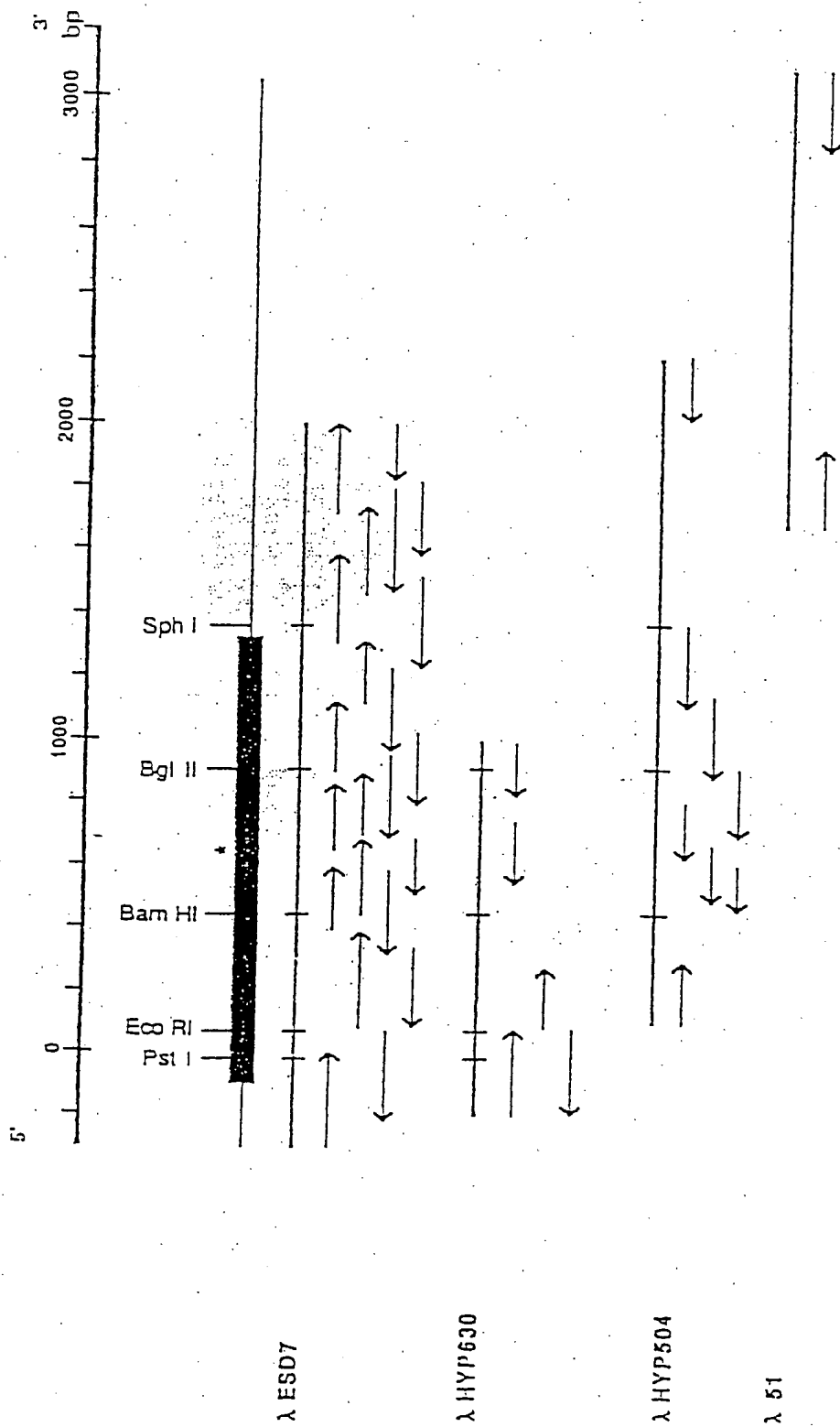


FIG. 21A

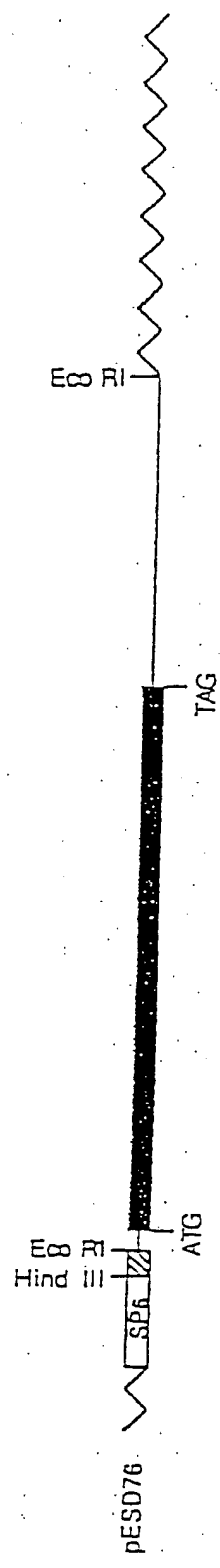


FIG. 21B



FIG. 22A

FIG. 22A



150
Gln Asn Cys Ser Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly Thr Met Val Asp Leu Ile 160
CAG AAC TGC TCG ATG AAG TTT GGA TCC TGG ACT TAC GAC GGT ACC ATG GGT GAC CTC ATT CTA ATC AAT GAA AAC Gln Asn Glu Asn Val Asp Arg Lys Asp 170
440 " 460 500
180
Phe Phe Asp Asn Gly Glu Trp Glu Ile Leu Asn Ala Lys Gly Met Lys Gly Asn Arg Arg Glu Gly Phe Tyr Ser Tyr Pro Phe Val Thr 200
TTT TTT GAT AAC GGA GAG TGG GAG ATA CTC AAC GCA AAG GGG ATG AAG GGC AAC AGA AGA GAA GGC TTT TAC TCC TAT CCG TTT GTT ACC
520 540 560 580 600
210
Tyr Ser Phe Val Leu Arg Arg Leu Pro Leu Phe Tyr Thr Leu Phe Leu Ile Ile Pro Cys Leu Gly Leu Ser Phe Leu Thr Val Leu Val 230
TAC TCT TTT GTC CTG ACA GGC CTG CCC TTG TTT TAC AGC CTC TTT TTG ATA ATA ATC CCC TGC CTG GGG TTG TCT TTT CTC ACG GTC CTG GTG
620 640 660 680
240
Phe Tyr Leu Pro Ser Asp Glu Gly Glu Lys Leu Ser Leu Ser Thr Ser Val Leu Val Ser Leu Thr Val Phe Leu Leu Val Ile Glu Glu 260
TTC TAC CTA CCC TCG GAC GAA GGG GAA AAA CTC TCA TTA TCC ACC TCC GGT TTG GTC TCT TTG ACG GTG TTT CTT TTA GTG ATT GAA GAA
700 720 740 760
270
Ile Ile Pro Ser Ser Lys Val Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Ile Met Ile Phe Val Thr Leu Ser Ile Ile Val Thr 290
ATA ATC CCG TCC TCT TCG AAG GTC ATC CCC CTC ATT GGC GAG TAC CTC CTC Tyr Leu Ser Ile Ile Val Thr Val Thr Leu Ser Ile Ile Val Thr
800 820 840 860
300
Val Phe Val Ile Asn Val His His Arg Ser Ser Thr Tyr Thr His Pro Met Ala Pro Trp Val Lys Arg Leu Phe Leu Gln Arg Leu Pro 320
GTT TTT GTA ATT AAT GTC CAC CAC AGA TCT TCC TCA ACG TAC CAT CCC ATG GCC CCC TGG GTG AAG AGG CTG TTT CTA CAA AGA CTC CCG
880 900 920 940 960
330
Arg Trp Leu Cys Met Lys Asp Pro Met Asp Arg Phe Ser Phe Pro Asp Gly Lys Glu Ser Asp Thr Ala Val Arg Gly Lys Val Ser Gly 350
AGA TGG CTT TGC ATG AAG GAC CCC ATG GAC CGC TTC TCT TTC CCG GAT GGA AAG CAG AGT GAT ACA GCC GTG AGG GGG AAA GTC TCA GGC
980 1000 1020 1040

FIG. 22B



Lys Arg Lys Gln Thr Pro Ala Ser Asp Gly Glu Arg Val Leu Val Ala Phe Leu Glu Lys Ala Ser Glu Ser Ile Arg Tyr Ile Ser Arg
AAA AGG AAA CAG ACT CCC GCC AGC GAT GGA CAA AGA GTT CTG GTC GCT TTC CTC CAG AAG GCC TCC GAG TCC ATC AGA TAC ATT TCG AGG
1060 1100 1120 1140

His Val Lys Lys Glu His Phe Ile Ser Gln Val Val Gln Asp Trp Lys Phe Val Ala Gln Val Leu Asp Arg Ile Phe Leu Trp Leu Phe
CAT GTG AAA AAG GAA CAC TTC ATC AGC CAG GTA GTG CAA GAC TGG AAA TTT GTG GCT CAA GTT CTG CAC CGC ATC TTC CTG TGG CTC TTT
1160 1200 1220 410

Leu Ile Ala Ser Val Leu Glu Lys Ile Phe Ile Pro Ala Leu Lys Met Trp Ile His Arg Phe His
CTG ATA GCT TCT GTG TTG GGT TCC ATT CTG ATT TTT ATT CCA GCC TTG AAG ATG TGG ATA CAT CGT TTC CAC TAG GAGCCACTCTCTGGACCCA
1240 1300 1320

TTTAGAGACATACATAGAGACAAATCCCACTTAGGACTGACAGCGGCTGGCATGCTCAGAGGACAGCCATGCAATGCTAGTGGTGGCCCTGTCTTGTCTGGAGCTTTCTGTG
1340 1360 1380 1400 1420 1440

ATTGCAGGGCACTGACAGAATCTGGGTTTGAGTTAGTGCATGATGGTGGCTGCCATTACAGGTGTAGTTGGGCAATTTGCGAGACGCTCTCCATGTTATTTATGTTGGGAGTTCTCTGAAC
1460 1480 1500 1520 1540 1560

TACTCCCTCTGCTCATCCCTCAACGCCACTGGGGCTATGTGTTATTTCTAGCAGTGTGGCTCAACGCCATTTTCACAATAGTTTCAGGAAATTAGCCAGGTACAACTCTCCACACACAGG
1580 1600 1620 1640 1660 1680

TCAAATTGCCACTGTGCAACGAGTCTCCACAAATAGGGTCAATTGAAGATGACCTTGAATGGCTATGACAGTTCTCTPAAGGAGGTGTTACTGGAAGTTTGTCTCACTGACCTGCGAAG
1700 1720 1740 1760 1780 1800

TTTTCGAATCCAGGTAGGAACCTGGGCTGATTTCTAGCTTGGCTGTAGGTTCCATCAAAATAGTTACCCCAAGAAAGCCATTGCGTAGTACAACTGTATTATTACACACATCTC
1820 1840 1860 1880 1900

TTTTTTTCCC.....J'
1930

FIG. 22C

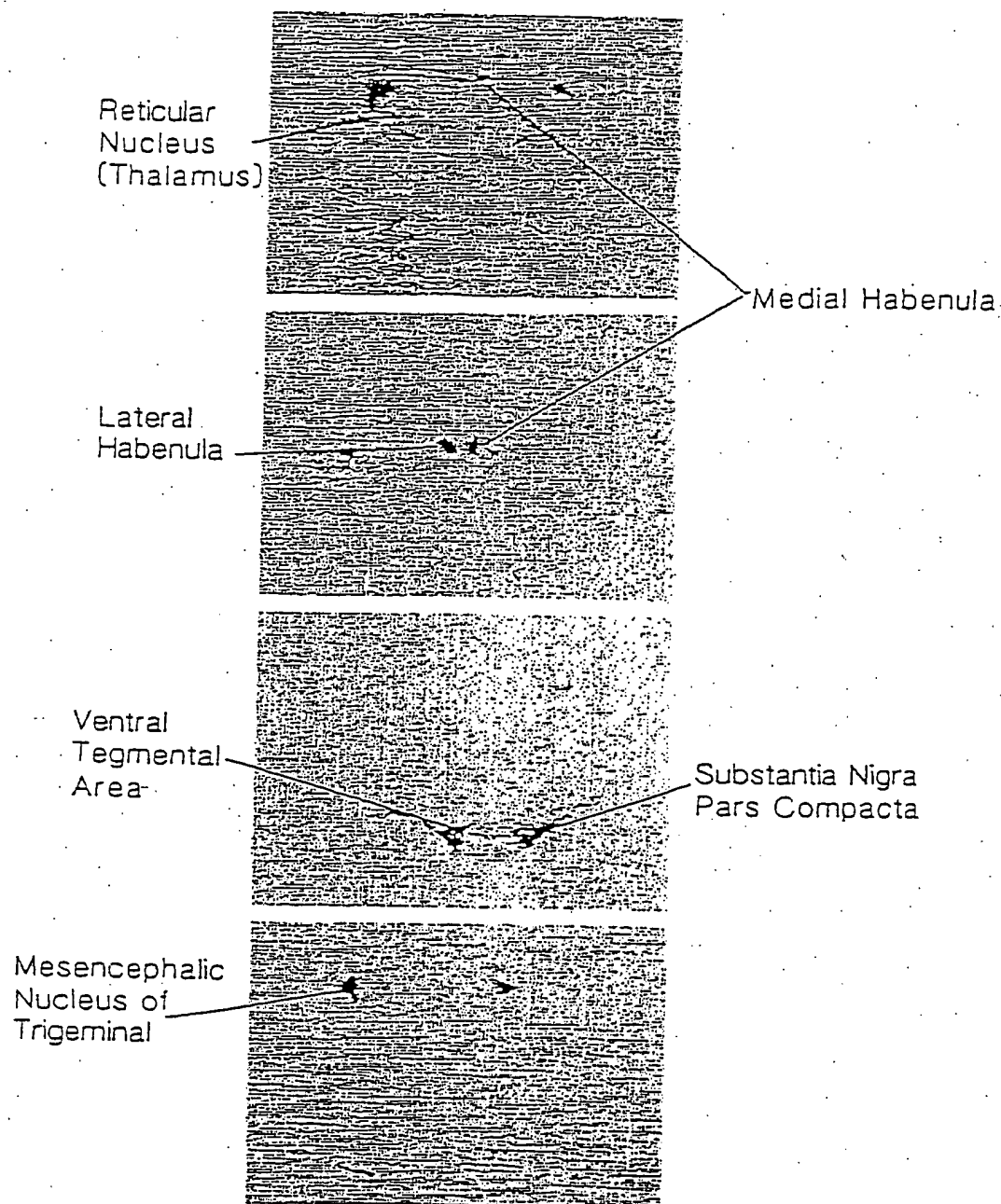


FIG. 24



FIG. 25

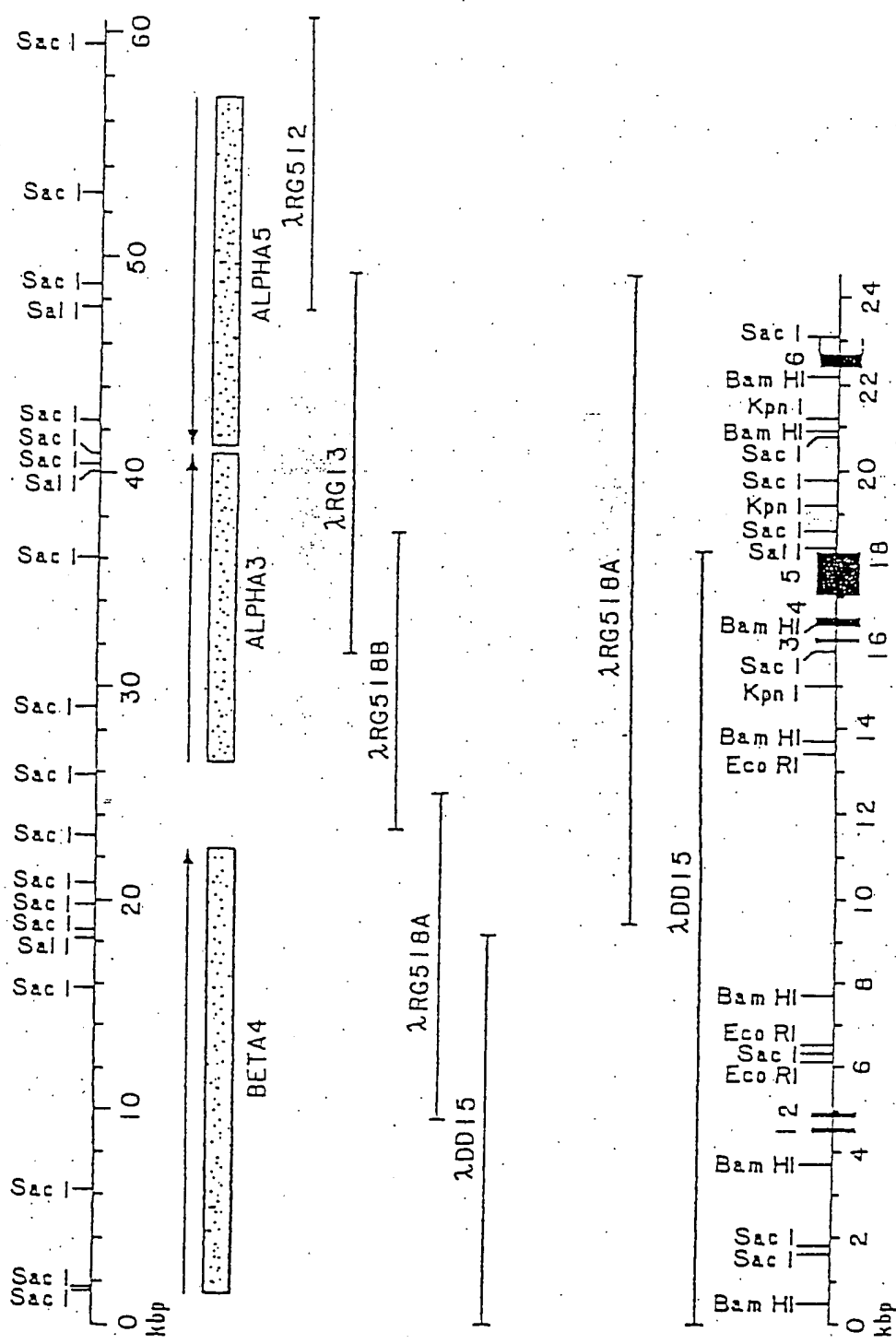


FIG. 26



5'...GCCAACCGGACAT -120

ACGCTCACTCGCGGTTCCATTGTAGACTGACCGGCTGCGACCCCGGCTGGCC -100
Met Arg Gly Thr Pro Leu Leu Leu Val Ser Leu Phe Ser Leu Leu Gln Asp
-20
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130 Ala Ile Tyr Lys Ser Ala Cys Lys Ile Glu Val Lys His Phe Pro Phe Asp 140
 GCT ATC TAC AAG AGT GCC TGC AAG ATT GAG GTG AAG CAC TTT CCC TTC GAC CAG AAsn Cys Thr Leu Lys Phe Arg Ser Trp Thr Tyr
 380 400 420 440
 160 Asp His Thr Glu Ile Asp Met Val Leu Lys Ser Ala Thr Ala Ile Met Asp 170
 GAC CAC ACG GAG ATT GAC ATG GTT CTT AAG TCG CCC ACG GCC ATC ATG GAT GAC TTC ACC CCC AGT GGT GAA TGG GAC Ile Val Ala Leu
 480 500 520 540
 190 Pro Gly Arg Arg Thr Val Asn Pro Gln Asp Pro Ser Tyr Val Asp Val Thr 200
 CCA GGA CGG AGG ACG GTG AAC CCT CAG GAC CCC AGC TAC GTG GAC GTG ACC TAT GAC TTC ATC ATC AAG CGC AAC GCG CTC Tyr Thr
 560 580 600 620
 220 Ile Asn Leu Ile Ile Pro Cys Val Leu Ile Thr Ser Leu Ala Ile Leu Val Phe 230
 ATC AAT CTT ATC ATT CCT TGT GTG CTC ATC ACC TCG CTG GCT ATC CTG GTC TTC TAC CTG CCC TCC GAC TGT GGG GAG Met Thr Leu
 660 680 700 720
 250 Cys Ile Ser Val Leu Leu Ala Leu Thr Phe Phe Leu Leu Leu Ile Ser Lys 260
 TGC ATC TCT GTG CTG CTG GCA CTC ACG TTC TTC CTG CTG CTC ATC TCC AAG ATC GTG CCT CCC ACC TCC CTT GAC ATA CCG CTC ATT GGC
 740 760 780 800
 280 Lys Tyr Leu Leu Phe Thr Met Val Leu Val Thr Phe Ser Ile Val Thr Thr 290
 AAG TAC CTC TTG TTC ACC ATG ATG GTG CTC GTC ACC ITT TCC ATG GTC ACC ACT GTG TGT GTG CTC AAT CTG CAC CAC CAC Ser Pro Ser Thr
 840 860 880 900
 310 His Thr Met Ala Ser Trp Val Lys Glu Cys Phe Leu His Lys Leu Pro Thr Phe 320
 CAC ACC ATG GCA TCC TCG GTC AAG GAG TGC TTC CTG CAC AAA CTG CCC ACC TTC CTC TTC ATG AAG CGT CCC GGT CTT GAA GTC AGC CTG
 920 940 960 980

FIG. 27B



340
Val Arg Val Pro His Pro Ser Gln Leu His Leu Ala Thr Ala Asp Thr Ala Ala Thr Ser Ala Leu Gly Pro Thr Ser Pro Ser Asn Leu
360
370
Tyr Gly Ser Ser Met Tyr Phe Val Asn Pro Val Pro Ala Ala Pro Lys Ser Ala Val Ser Ser His Thr Ala Gly Leu Pro Arg Asp Ala
390
TAT GGG AGT TCC ATG TAC TTT GTG AAC CCT GTC CCT GCC GCT CCT AAG TCT GCA GTC ACC TCC CAC ACA GGC CTC CCC AGG GAT GCC
1100
1120
1140
1160
1180
1200
Arg Leu Arg Ser Ser Gly Arg Phe Arg Glu Asp Leu Gln Gln Ala Leu Glu Gly Val Ser Phe Ile Ala Gln His Leu Glu Ser Asp Asp
420
CGT CTC AGG TCC TCC GGG AGG TTC CCG GAA GAT CTA CAG GAA GCA TTA GAG GGT GTC AGC TTC ATC GCC CAG CAT CTG GAC AGC GAT GAC
1240
1260
Arg Asp Gln Ser
CGA GAT CAA AGT gtatgtactg...
430
Val Ile Glu Asp Trp Lys Phe Val Ala Met Val Val Asp Arg Leu Phe Leu Trp
440
...ttgtctgseq GTC ATC GAG GAC TGG AAG TTC GTC GCG ATG GTT GTT GAC CGC CTC TTC CTG TGG
1300
1320
Val Phe Val Phe Val Cys Ile Leu Gly Thr Met Gly Leu Phe Leu Pro Pro Leu Phe Gln Ile His Ala Pro Ser Lys Asp Ser
450
GTG TTC GTG TTT GTG TGT ATT CTG GGC ACC ATG GGG CTC TTC CTG CCA CCC GTT TTC CAG ATC CAC GCA CCC TCC AAG GAC TCC TAG GCT
1340
1360
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1400
1420
ACCCGGCITGTCGGGHHCCGGGAAAGTAGTAGATGATATGAGAACGGGTGGGAGCAGGGCGTGTCTTTGGGCTACCCGGGCTGTCTCGGGCCCGGGGAAAGTAGTAGATATGA
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GAAAGCGGTGGGAAAGCAGGGCGTGTCTTCGG...J'
1540

FIG. 27C

[illegible]

FIG. 28A

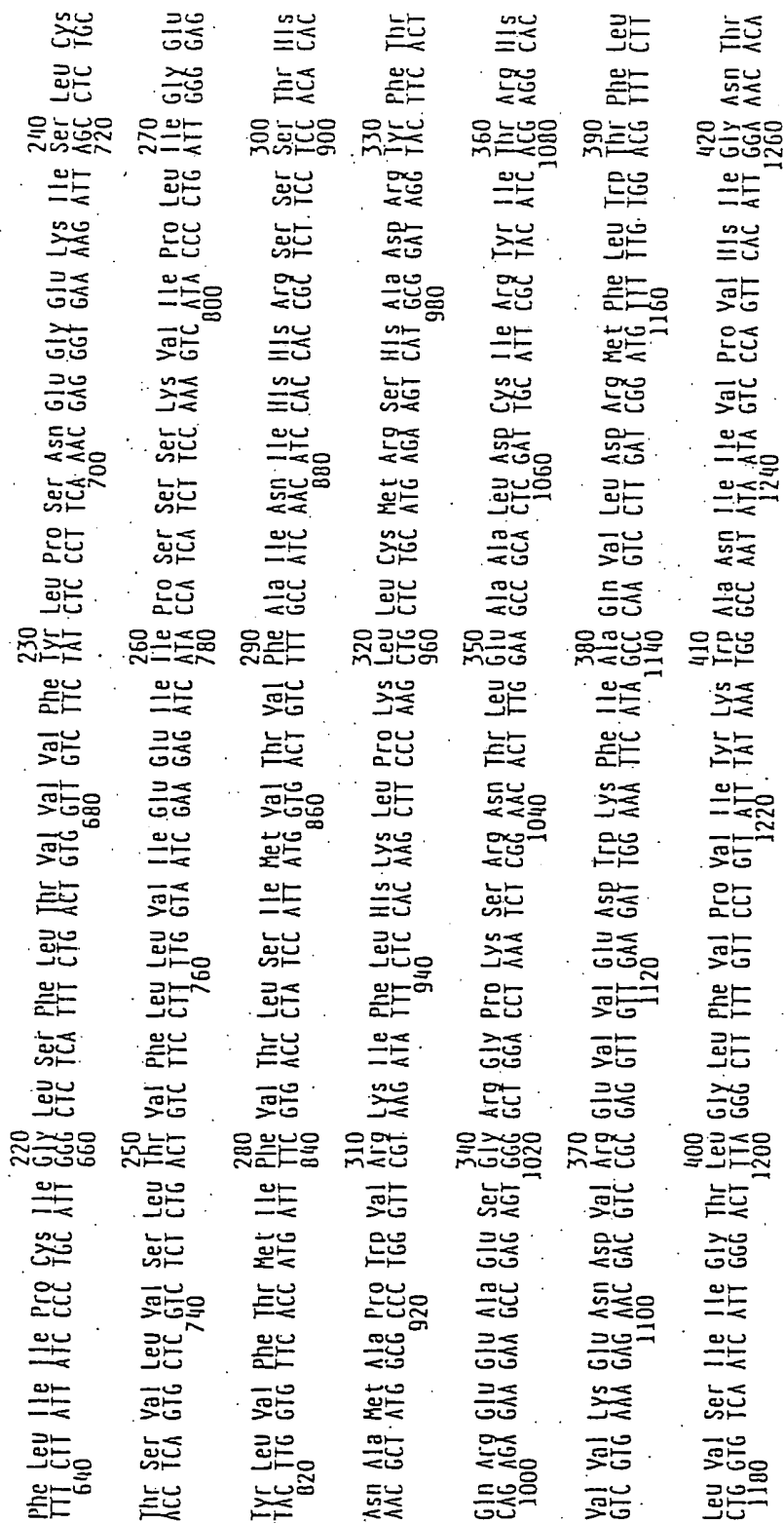


FIG. 28B



11e LYS
ATT AAG TGA ACCAAGAAATTACCCTGTGGATTAGTGAGCAGTCATGCAGCTCTTAGGACATGTATGCTGTTATGGAAATGTGAAGGTAGTTACAAATTGACATAGGCTATAACA
1280 1300 1320 1340 1360 1380
GATTAGCAATTTCTAACATTTGGCTTAATGTTGTCCATTAGAACTGCAGTAATAACCTCAAAATAGCAACAACACATTTGCTGCCTGCACCTAGTGAAGGCCCTAGCAATCCTGGCAA
1400 1420 1440 1460 1480 1500
ACCCTAECMAATTTGCAACCAATGATGAAGGCCATCCTTTGGAGTGCTGGAAACTCAACTGTATTGAAGACTATTTAAACTCCCCCAAAATTTAGTAGGAACAATATATGTGTGGTT
1520 1540 1560 1580 1600 1620
TTGAATTTTCAGAAATGGGCTTTGGGCTTGTAAATTTGCTGGGCTAGCACAAAACCTCCTGAGTAGCTGGGACCAATGGGTGTCTGCACCTTTGCCCCCTGTTCTGTATTTCACAGATATA
1640 1660 1680 1700 1720
AAATACATCATTTTATAGGAGGTAGGCCCATTTACTTGGTTTAATAATAACTTAATGTCAGTTAGGTTTAATTATAACCTTATGTCAGCTAATGTTCTATTGCTGTGAAGAGACATC
1760 1780 1800 1820 1840
ATGACCATCAACTCTTATAAAGAAACATTTTCATCAGTGGCTGGCTTACAGTTTTTGGAGGTTTAGCCAAATTCACAGTGAAGCATGATAGCATCCAGGTAGACATAATGCTGGATCC
1880 1900 1920 1940 1960
AGGAGTTCCTACATCTGGATCAGCAGGCGAGGAGAGAGAGGCCACTGGACCTGGCTTGAGCATCTGAAACCTCAAGCCCCACCTCCAGTGACACACCTTCCCCCAACAAAGGCC
2000 2020 2040 2060 2080
ACACCTCCTAATAGTGCCACTTGGCTGGTCAAGCATTCAGTCTATGGGTCTACGAGAGGCCATTTCCTATTCAAAACACACACTTAATAGGATGCTATTCTTTACTGACATTTTAAATAAG
2100 2120 2140 2160 2180 2200
CGACAAATGGTAACTAGAAACATCGTAGGCCACTTTACTCTTTTATATGGTAAATATGGATTGGCTTTTATATTAAGTTTACAGCCTATCTGAAACATGTAACAGGCAACTCCTG
2220 2240 2260 2280 2300 2320
CAGACACATTTCTTTGTAATGACTTTTATAATCTCGCAGTGGCATGTTCTGGTAATGACTTCAGTCTCCTCGTCCACACTCTCGGTTAGTAGAGCCATTATATGTATCATCGCGTATCCCTG
2340 2360 2380 2400 2420 2440
ATTTCAGAGCAACTGTGTCAGTTGCACAGGTTCCCACTCAAAATGGGATGCCATGACTCTGTCTGGATAATTTCTGTGGAAACCACTTCTGAGCTGGATACGGTGGCTCATACCTGTCA
2460 2480 2500 2520 2540 2560
TGCTACTTTTCAGGAGGCGAGGCGAATTGCTGTGAGTTGTTGGTCAGCCTGGGTACATATGAGACCCCTGTCTCAGAAACCAAAACAAACAAACCTTCCCCCTGTGAGTTGATATAAG
2580 2600 2620 2640 2660 2680
CACACTGTATATCCGAATTTGGGGATCCCTCTAGAGTCGACCTGCAGGCATGCAAGCTTGGGCTAATCATGGTCATAGCTGTTCCCTGTGTGAATGTTATCCG
2700 2720 2740 2760 2780

FIG. 28C



BITA2 HLACHAGHSUSHALFSLLMLCSGVLGTDEERLVEHLLDPSSYHKLIRPATNGSELVTQVHVSQAQLISVHEREQINTIIVHLTOEHWEDYHLTWKPEDFOHKK
BITA3 HTGFLRVFLVLSATLSGSWVTLTATAGLSSVAEHEDALLRHLTOGYQKVPVPLNSSDIKVYGLKISQVLDVDEKHQLHTTHVHLKQEHTDOKLRHNPPEEYGGIH
BITA4 HRGTFLLLVSLFSLLOQGDCLAHAEKXMDLLMKTRYHNLIRPATSSQLISIRLELSQLISVHEREQINTISHLKQEHTDYRLAHNSSCYEGVH
----- SIGNAL PEPTIDE -----

BITA2 KVLRLPSKHIMLPDVLVYHHADGHVEVSFYSHAVSVYDGSIFHLPPAIYKSACKIEVHHFPDQOQHCTHKFRSHTYDTEIDLVLKSDVASLDOFTPSGEMOIIALPG
BITA3 SIKVPSSESLHLPDIVLFENADGHEGSLHTKAIKSSGTVSWTPPASYSKSSCTHDVTFPPDRQHCSHKTGSMTYDGTHTVDLILTHEWVRKDTFGONGEWEILHANG
BITA4 ILRIPAKRVWLPDIVLYHHADGHVEVSVYTHIVRSNGSIOHLPPIYKSACKIEVHHFPDQOQHCTLKRFSWTYDTEIDHVLKSATAIHODITPSGEMDIVALPG

BITA2 RMENPDOS TYVOITYDGTIRKPLFYTHLITPCVLITSLAILVFLPSDCGEMHTLCISVLLALTIVFLLLISKIVPPTSLDVLVGVKYLHFTHVLTIVTSV
BITA3 HKGHRREGTYSYFVTVSYFVLRRLPLFYTLFLIIPCLGLSFLTVLVFLYLPDSDEGKLSLSTSLVSLTVLLVIEEITPSSKVIPLIGEYLLFINIFVLSIIVTV
BITA4 RRTVUPDP SYDVTYDGTIRKPLFYTHLITPCVLITSLAILVFLYLPDSDCGEMHTLCISVLLALTIVFLLLISKIVPPTSLDVLVGVKYLHFTHVLTIVTSV
----- MSR I ----- MSR II ----- MSR III -----

BITA2 CVLHVHHRSPPT HTHAPWVKVVFLEKPLTLLTLOQPRHRCARQLRLRRQRERECEAVTFREGPAADPCSVGPCSCG
BITA3 FVIVVHHRSSSTYBPHAPWVKRLFLQRLPMLCHKDPHDTGSPDCKESDTAVRGVSGXKQTPASDGERVLVAFLEK
BITA4 CVLHVHHRSPST HTHASHVKECFLHKLPTTLPHKRPGLVSLVRVPHPSQLHATADTAATSALGPTSPSHLYGSSHYGVHPVPAAPKSAVSSITAGLPRDANLRS

BITA2 LREAVDGVRFIADHHRSEDDQSVREDMKYVAHVDRFLFLNIFVFCVGTGVGHFLOPLQHYTATTLHPDHSAPSSK*
BITA3 ASESYRISNVKKEHFIQVVDQDKFVAQVLDRIFLFLIASVLGSLIFIPALKHNRFH*
BITA4 SGRFREDLQEALEGVSFIAONLESDDRDQSVIEDMKFVAHVDRFLFLVAVFVFCILGTHGLTLPFLQIHAPSODS*
----- MSR IV -----

FIG. 29

ALPHA2 HTLSHALQFMTHLYLWCLLLVPAVLTOQCSHTHAEDRLFKHLTGGYHNRHARVPVPHTSDDVIVRGLSIAQLIDVDEKIQHMTTHVHLKQEHNOYKLRKOPAE
 ALPHA3 HGVVLLPPPLSHLHLVHLPLPAASASEAENHLFOYLFEDYNEIIRPVAHVSHPVIIQFVSHSGLVKVDEVQIHETHLKQIWHYOYKLRKPPSO
 ALPHA4 HEIGGPCAPPFLLLPLPLLLGLTGLLPASSHIEIETRAHAEELLKRLFGSYHKSAPVGHISDVLVNFRGLSIAQLIDVDEKIQHMTTHVHLKQEHNOYKLRKOPAE
 ALPHA5 HVQLLAGNRPTGARRGTAGGLPELSSAAXKHEDSLFRDLFPEDYERHVRPVEHLSQKIKINFGLAISQLVDVDEKIQHMTTHVHLKQEHNOYKLRKOPAE
 _____ SIGNAL PEPTIDE _____

ALPHA2 FGNVTSLRVSEHIIPOIVLYNHADGEFAVTHNTKXHLFFTGTVHNVPPAIYKSSCSIDVTFPPDQOCHKHFGSHTYDKAKIDLEQHMTTHVHLKQEHNOYKLRKOPAE
 ALPHA3 YOGVEFHRVPAEKIMKPOIVLYNHADGDFQVDDKTALLIKYTGVEVTHIPPAIKSSCKIDVTFPPDQOCHKHFGSHTYDKAKIDLEQHMTTHVHLKQEHNOYKLRKOPAE
 ALPHA4 YEHVTSIRIPSELIWRPOIVLYNHADGDFAVTHLTKAHLFYDGRVOTPPAIYKSSCSIDVTFPPDQOCHKHFGSHTYDKAKIDLEQHMTTHVHLKQEHNOYKLRKOPAE
 ALPHA5 YGGIKIIRVPSDSLHIIPOIVLYNHADGDFEGAS TKTVVRYHGTVTHTQPAHYKSSCTIDVTFPPDQOCHKHFGSHTYDKAKIDLEQHMTTHVHLKQEHNOYKLRKOPAE

ALPHA2 IIMATGYHNSKKYDCCAEIYPDVTVYVIRRLPLFYTHLIIIPCLLSCLTVLVYLPSECGEKITLISVLLSLTVLFLLLITEIIPSTSLVPLIGEYLLFTTHIF
 ALPHA3 IIKAPGYKHEIYHCCCEIYQDITVLSYIRRLPLFYTHLIIIPCLLSCLTVLVYLPSECGEKITLISVLLSLTVLFLLLITEIIPSTSLVPLIGEYLLFTTHIF
 ALPHA4 IVDVAGTYHTRKYECCEIYPOITVAFIIRRLPLFYTHLIIIPCLLSCLTVLVYLPSECGEKITLISVLLSLTVLFLLLITEIIPSTSLVPLIGEYLLFTTHIF
 ALPHA5 IMSHSGKHRTDSCCH YPIITVSFVIKRLPLFYTHLIIIPCLLSCLTVLVYLPSECGEKITLISVLLSLTVLFLLLITEIIPSTSLVPLIGEYLLFTTHIF
 _____ MSR I _____ MSR XI _____ MSR XII _____ MSR XIII

ALPHA2 VTLSIVITVFLVHIVHRSPTTHHPPH HVRVALLGRVPRHLMHHRPLPPHELHGSPDLKLSPSYHMLTTHMDAGEREETEETEEEEEEDENICVCAGLPDSSSHCVLYG
 ALPHA3 VTLSIVITVFLVHIVHRSPTTHHPPH HVRVALLGRVPRHLMHHRPLPPHELHGSPDLKLSPSYHMLTTHMDAGEREETEETEEEEEEDENICVCAGLPDSSSHCVLYG
 ALPHA4 VTLSIVITVFLVHIVHRSPTTHHPPH HVRVALLGRVPRHLMHHRPLPPHELHGSPDLKLSPSYHMLTTHMDAGEREETEETEEEEEEDENICVCAGLPDSSSHCVLYG
 ALPHA5 VTLSIVITVFLVHIVHRSPTTHHPPH HVRVALLGRVPRHLMHHRPLPPHELHGSPDLKLSPSYHMLTTHMDAGEREETEETEEEEEEDENICVCAGLPDSSSHCVLYG

ALPHA2 HGGLHRAHEPETKTPSOA
 ALPHA3 TRSSSESVMHVL
 ALPHA4 TCRSPPLEVPLKNTSEVENXASPCBPSCPPPKSSSGAPHILIKARSLVQHVPSSQEAEDGIRCSNRSIOYCVSODGAAASLADSKPTSSPTSLKARPSQLPVSDQ
 ALPHA5

ALPHA2 SKLLSPQIOKALEGVHVIADRLRSEDADSSVKEDWKYVAHVVDRIFLHLFIIVCFLGTIGLFLPPFLAGHI*
 ALPHA3 SLALSPEIKAEIQSVKVIYAEHKKXONVAKIEQDDWKYVAHVVDRIFLHLFIIVCFLGTIGLFLPPFLAGHI*
 ALPHA4 ASPCKGCTCKEPPSPVPTVLKAGGTAKAPPQIPLSPALTRAVEGVQIADHLKAEEDTDFSVKEDWKYVAHVVDRIFLHLFIIVCFLGTIGLFLPPFLAGHI*
 ALPHA5 LEAALDCIRYITRHHVVKENDVREVEEDWKIEAQLONLMTLFTLLVSIIGTLGLFVVPVFIINGPI*
 _____ MSR IV _____

FIG. 30

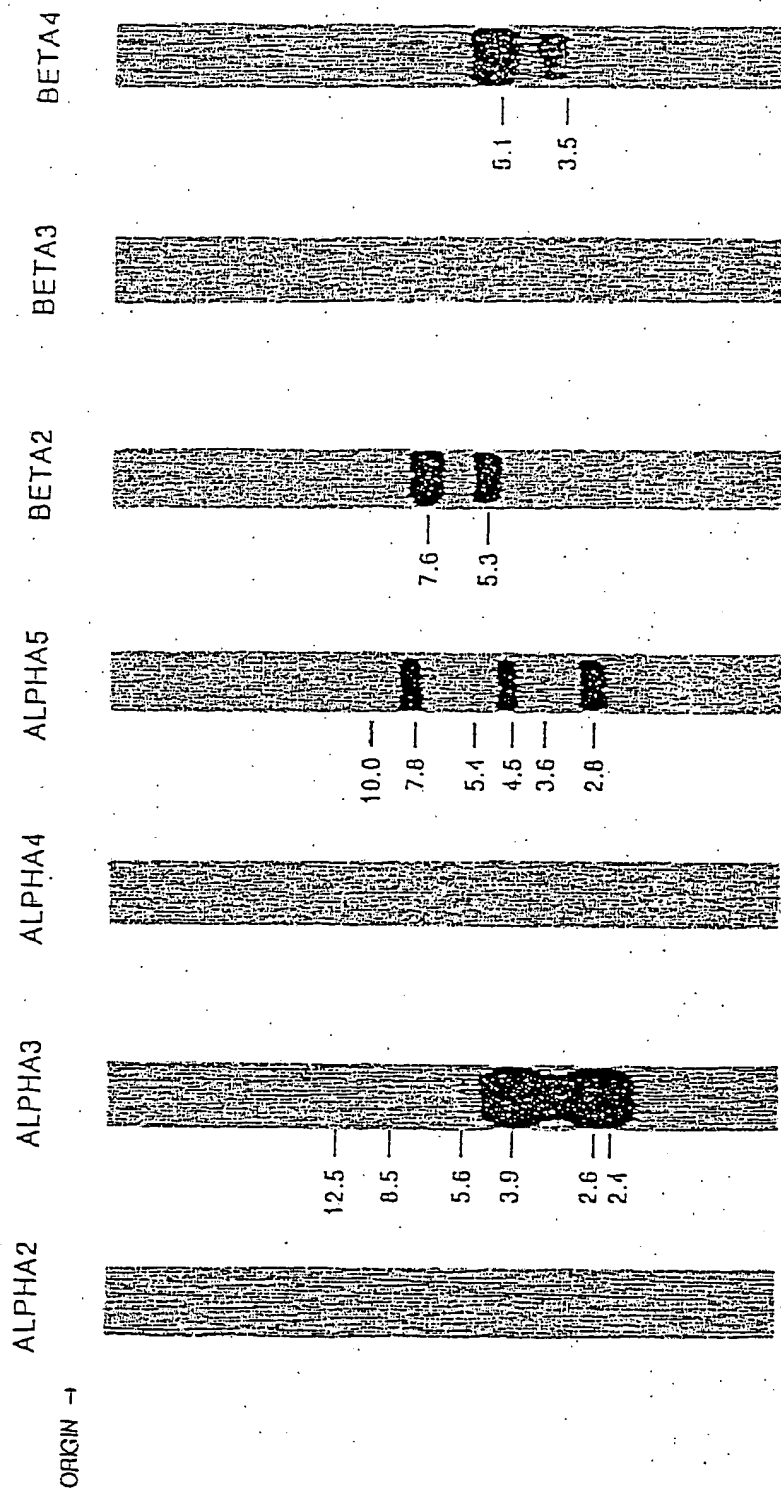


FIG. 31

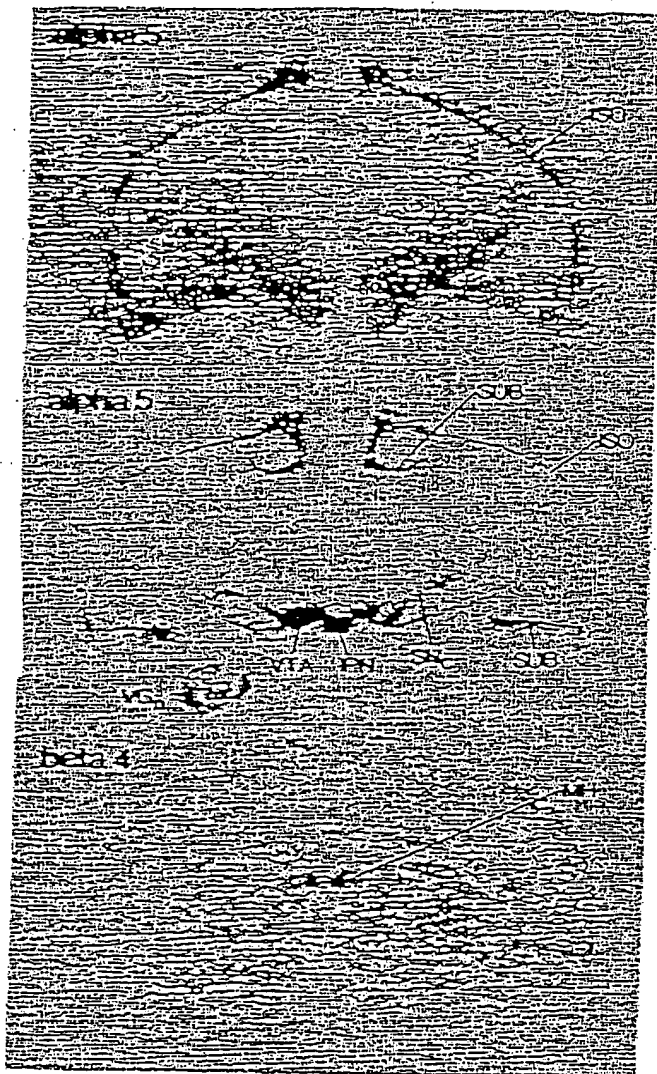


FIG. 32